

OM protein - protein search, using sw model
Run on: February 7, 2006, 16:21:51 ; Search time 203 Seconds
(without alignments)
575.738 Million cell updates/sec

Title: US-10-006-867-2
Perfect score: 1392
Sequence: 1 MWFFQGLSFLPSALVWTS.....YDTAPCPINNETRLLSRDI 266
Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description

RESULT 1
ID AAY66636 standard; protein; 266 AA.
DE Membrane-bound protein PRO180.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;

RESULT 2
ID AAU79028 standard; protein; 266 AA.
DE Human PRO polypeptide sequence #5.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;

RESULT 3
ID AAM39568 standard; protein; 266 AA.
DE Human polypeptide SEQ ID NO 2713.
PN WO200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1392; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;

RESULT 4
ID AAB65159 standard; protein; 266 AA.
DE Human PRO180 (UNQ154) protein sequence SEQ ID NO:23.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;

RESULT 5
ID ABB90338 standard; protein; 266 AA.
DE Human polypeptide SEQ ID NO 2714.
PN WO200190304-A2.
PD 29-NOV-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 5; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 6
ID ABG95851 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.

PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 5; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 7
ID ABUS8404 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 8
ID ABUS7952 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 9
ID ABUS4267 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 10
ID ABR66141 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 11
ID ABR65531 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 12
ID ABUS99471 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 13
ID ABUS7974 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 14
ID ABUS9052 standard; protein; 266 AA.
DE Novel human secreted or transmembrane protein PRO180.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 15
ID ABUS2564 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 16
ID ABUS2710 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032113-A1.

PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 17
ID ABU89831 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 18
ID ABR68080 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 19
ID ADA57044 standard; protein; 266 AA.
DE Human secreted protein #327.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 20
ID ABU60483 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, #9.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 21
ID ABU96133 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 22
ID ABU92564 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 23
ID ABO08641 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044323-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 24
ID ABO02693 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 25
ID ABR74847 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 26
ID ABR94609 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 27
ID ABU13865 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 28
ID ABU85582 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 29
ID ABU98742 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 30
ID ABU97957 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 31
ID ABU91663 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 32
ID ABU89356 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 33
ID ABU86197 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 34
ID ABU67410 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 35
ID ABU80438 standard; protein; 266 AA.
DE Human PRO protein #5.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 36
ID ABU72450 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 37
ID ABUS0876 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 38
ID ABO33935 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 39
ID ABR99356 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 40
ID ABR98746 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 41
ID ABO16269 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 42
ID ABR92169 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 43
ID ABO18810 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044325-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 44
ID ABR78231 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 45
ID ABOU71952 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 46
ID ABO19115 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

ID ABUS94967 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 47
ID ABO00106 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 48
ID ABO11438 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 49
ID ABO02083 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 50
ID ADA40898 standard; protein; 266 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 51
ID ABUS8657 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 52
ID ABUS3352 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 53
ID ABO06153 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 54
ID ABR59189 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 55
ID ABO09251 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 56
ID ABO19115 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 57
ID ABO11133 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 58
ID ABR66751 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 59
ID ABO15964 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 60
ID ABO13670 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 61
ID ABO171506 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 62
ID ABO65573 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, SEQ ID 10.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 63
ID ABO07421 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 64
ID ABO03608 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 65
ID ABR67056 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 66
ID ABO13980 standard; protein; 266 AA.
DE Novel human secreted protein #9.
PN US2003028003-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 67
ID ABO15659 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054483-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 68
ID ABO55940 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, PRO180.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 69
ID ABO72287 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 70
ID ABO65268 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 71
ID ABO95213 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 72
ID ABO71116 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 73
ID ABO07726 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 74
ID ABR69967 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003028003-A1.

PN US2003032138-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 75
 ID ABR69300 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003036132-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 76
 ID ABO01441 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US200308353-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 77
 ID ABR61243 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003017542-A1.
 PD 23-JAN-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 78
 ID ABR60040 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003032137-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 79
 ID ABU90960 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003018168-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 80
 ID ABR67775 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003027269-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 81
 ID ABR65163 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003027268-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 82
 ID ABR68385 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003027274-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 83
 ID ABR71797 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003032135-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 84
 ID ABU59199 standard; protein; 266 AA.

DE Human secreted/transmembrane protein, #9.
 PN US2003027162-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 85
 ID ABU85277 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2003022295-A1.
 PD 30-JAN-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 86
 ID ABU88967 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003022297-A1.
 PD 30-JAN-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 87
 ID ABU83047 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003032105-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 88
 ID ABU94903 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003032123-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 89
 ID ABU90451 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003032108-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 90
 ID ABU83962 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003032111-A1.
 PD 13-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 91
 ID ABU93613 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003032119-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 92
 ID ABO25896 standard; protein; 266 AA.
 DE Human PRO180 polypeptide.
 PN US2002127576-A1.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 93
 ID ABR64858 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003027263-A1.
 PD 06-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 94
 ID ABO27281 standard; protein; 266 AA.
 DE Human secreted/transmembrane polypeptide PRO180.

PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 95
ID ABR68690 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 96
ID ABO06506 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 97
ID ABR99051 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 98
ID ABUS6935 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 99
ID ABUS8587 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 100
ID ABUS2174 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 101
ID ABUS7185 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 102
ID ABUS3657 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 103
ID ABO08031 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 104
ID ABUS2476 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003045684-A1.
PD 06-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 105
ID ABUS1742 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 106
ID ABUS6506 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 107
ID ABUS1146 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 108
ID ABR59735 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 109
ID ABUS3923 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 110
ID ABUS9776 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 111
ID ABR66446 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 112
ID ABR90864 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 113
ID ABO53261 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 114
ID ABUS8905 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, #9.
PN US2002142961-A1.

PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 115
ID ABU94291 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 116
ID ABU79173 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 117
ID ABU86502 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 118
ID ABU86807 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 119
ID ABU94596 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 120
ID ABO04523 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 121
ID ABR70272 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 122
ID ABU92283 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 123
ID ABU98437 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 124
ID ABR65836 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 125
ID ABR64553 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 126
ID ABU59348 standard; protein; 266 AA.
DE Novel human secreted or transmembrane protein PRO180.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 127
ID ABU79478 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 128
ID ABU92869 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 129
ID ABU95828 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 130
ID ABU91048 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 131
ID ABU90141 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 132
ID ABO09556 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 133
ID ABO10828 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 134
ID ABR70882 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 135

ID ABU98263 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 136
ID ABU97490 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 137
ID ABU91358 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 138
ID ABU99268 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 139
ID ABU94572 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 140
ID ABR69662 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 141
ID ABU80039 standard; protein; 266 AA.
DE Human PRO protein #5.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 142
ID ABU82475 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 143
ID ABU92114 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 144
ID ABU93308 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 145

ID ABO09861 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 146
ID ABO08946 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 147
ID ABU96439 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 148
ID ABU10820 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 149
ID ABU10514 standard; protein; 266 AA.
DE Human secreted/transmembrane protein #5.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 150
ID ABU81572 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 151
ID ABU72109 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 152
ID ABU95523 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 153
ID ABU96732 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 154
ID ABR70577 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 155
ID ABO04928 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 156
ID ABO08336 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 157
ID AB088511 standard; protein; 266 AA.
DE Human secreted and transmembrane polypeptide PRO180.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 158
ID ABO34025 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 159
ID ABO05543 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 160
ID ABR73932 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 161
ID ABR95524 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 162
ID ABR80821 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 163
ID ABR81126 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 164
ID ABM00822 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 165
ID ABR88424 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 166
ID ABM77245 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 167
ID ABO28729 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 168
ID ABO31474 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 169
ID ABM07891 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 170
ID ABO40371 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 171
ID ABO35796 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 172
ID ABO43935 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 173
ID ADA77762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073180-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 174
ID ABR24730 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 175
ID ABO02998 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 176
ID ABR90254 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 177
ID ABM17168 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 178
ID ABR94914 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 179
ID ABR95219 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 180
ID ADB17059 standard; protein; 266 AA.
DE Human transmembrane PRO polypeptide (SeqID 2).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 181
ID ABO21457 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 182
ID ABR97721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 183

ID ABR87509 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 184
ID ABM77550 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 185
ID ABM27780 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 186
ID ABM06061 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 187
ID ABM03567 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 188
ID ABM35018 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 189
ID ABM26255 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 190
ID ABO48037 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 191
ID ABR92779 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 192
ID ABO24540 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.

PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 193
ID ADAJ37534 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 194
ID ABM11551 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 195
ID ABM02652 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 196
ID ABM15948 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 197
ID ABM27509 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 198
ID ABM29000 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 199
ID ABM06976 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 200
ID ABM21070 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 201
ID ABM09416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073175-A1.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 202
ID ABO41286 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 203
ID ABO36101 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 204
ID ABO43630 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 205
ID ABM76330 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 206
ID ABM76026 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 207
ID ABM25645 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 208
ID ABM25950 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 209
ID ADA21220 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO180.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 210
ID ABO03303 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 211
ID ABO02388 standard; protein; 266 AA.

DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003040061-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 212
 ID AB044239 standard; protein; 266 AA.
 DE Human secreted/transmembrane polypeptide PRO 180.
 PN US2003018172-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 213
 ID ABR90559 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003036130-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 214
 ID ABR73627 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003054468-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 215
 ID ABO16879 standard; protein; 266 AA.
 DE Human secreted/transmembrane protein (PRO) #5.
 PN US2003054470-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 216
 ID ABR94304 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003044917-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 217
 ID ABR75811 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003044529-A1.
 PD 06-MAR-2003.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 218
 ID ABR71187 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003059880-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 219
 ID ABR93084 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003064465-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 220
 ID ABR93389 standard; protein; 266 AA.
 DE Human secreted polypeptide PRO180, SEQ ID NO:10.
 PN US2003054478-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 6; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;

Best Local Similarity	100.0%;	Pred. No. 4.7e-149;
RESULT 221		
ID ADA10007 standard; protein; 266 AA.		
DE Human secreted/transmembrane protein, PRO180.		
PN US2003059831-A1.		
PD 27-MAR-2003.		
Query Match	100.0%;	Score 1392; DB 6; Length 266;
Best Local Similarity	100.0%;	Pred. No. 4.7e-149;
RESULT 222		
ID ABR87814 standard; protein; 266 AA.		
DE Human secreted polypeptide PRO180, SEQ ID NO:10.		
PN US2003068718-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1392; DB 6; Length 266;
Best Local Similarity	100.0%;	Pred. No. 4.7e-149;
RESULT 223		
ID ABO27814 standard; protein; 266 AA.		
DE Human secreted/transmembrane protein (PRO) #5.		
PN US2003064454-A1.		
PD 03-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1392; DB 6; Length 266;
Best Local Similarity	100.0%;	Pred. No. 4.7e-149;
RESULT 224		
ID ABO29949 standard; protein; 266 AA.		
DE Human secreted/transmembrane protein (PRO) #5.		
PN US2003064461-A1.		
PD 03-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1392; DB 6; Length 266;
Best Local Similarity	100.0%;	Pred. No. 4.7e-149;
RESULT 225		
ID ABO33158 standard; protein; 266 AA.		
DE Human PRO polypeptide #5.		
PN US2003068724-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1392; DB 6; Length 266;
Best Local Similarity	100.0%;	Pred. No. 4.7e-149;
RESULT 226		
ID ABO4846 standard; protein; 266 AA.		
DE Human secreted polypeptide PRO180, SEQ ID NO:10.		
PN US2003068727-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1392; DB 6; Length 266;
Best Local Similarity	100.0%;	Pred. No. 4.7e-149;
RESULT 227		
ID ABO8806 standard; protein; 266 AA.		
DE Human secreted polypeptide PRO180, SEQ ID NO:10.		
PN US2003068772-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1392; DB 6; Length 266;
Best Local Similarity	100.0%;	Pred. No. 4.7e-149;
RESULT 228		
ID ABO36406 standard; protein; 266 AA.		
DE Human secreted/transmembrane protein (PRO) #5.		
PN US2003068714-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1392; DB 6; Length 266;
Best Local Similarity	100.0%;	Pred. No. 4.7e-149;
RESULT 229		
ID ABO35491 standard; protein; 266 AA.		
DE Human PRO polypeptide #5.		
PN US2003068758-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1392; DB 6; Length 266;
Best Local Similarity	100.0%;	Pred. No. 4.7e-149;
RESULT 230		
ID ABO35491 standard; protein; 266 AA.		
DE Human PRO polypeptide #5.		
PN US2003068758-A1.		
PD 10-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1392; DB 6; Length 266;
Best Local Similarity	100.0%;	Pred. No. 4.7e-149;

ID ABO39456 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PD US2003068776-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 231
ID ABM10331 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 232
ID ABM11856 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 233
ID ABO52002 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PD US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 234
ID ABO52307 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PD US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 235
ID ADA19864 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PD US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 236
ID ABO23625 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PD US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 237
ID ADB17247 standard; protein; 266 AA.
DE Human transmembrane PRO polypeptide (SeqID 2).
PD US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 238
ID ADA17551 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PD US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 239
ID ABR97111 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003054481-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 240
ID ABR6899 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 241
ID ABM10941 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 242
ID ABM28085 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 243
ID ABO32084 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PD US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 244
ID ABM15211 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 245
ID ABM06366 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 246
ID ABM04177 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 247
ID ABM22290 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 248
ID ABM07586 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PD US2003068751-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 249
ID ABO40676 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 250
ID ABM35323 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 251
ID ABM33086 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 252
ID ABO52612 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 253
ID ABO50172 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 254
ID ABU99166 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 255
ID ABO4218 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 256
ID ABO05848 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 257
ID ABM18388 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 258
ID ADA27659 standard; protein; 266 AA.

DE Human secreted/transmembrane protein PRO180.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 259
ID ABR97416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 260
ID ABR80516 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 261
ID ABM01127 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 262
ID ABR88729 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 263
ID ABM13381 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 264
ID ABM20765 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 265
ID ABO41896 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 266
ID ABO42506 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 267
ID ABM10026 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003067478-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 268
ID ABO38541 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 269
ID ABM32781 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 270
ID ABM22595 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 271
ID ABM74806 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096333-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 272
ID ADA79554 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 273
ID ABR96196 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 274
ID ABM02347 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 275
ID ABR86289 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 276
ID ABR86594 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 277
ID ABM16558 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 278
ID ABM29610 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 279
ID ABO29034 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 280
ID ABM23815 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 281
ID ABM23205 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 282
ID ABM21985 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 283
ID ABO37626 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 284
ID ABM28390 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 285
ID ABM28695 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 286
ID ABM66339 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068737-A1.
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 287
ID ABM75721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 288
ID ABM34001 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 289
ID ABM34306 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 290
ID ABO20237 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 291
ID ABO21152 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 292
ID ABO22067 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 293
ID ADA20036 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 294
ID ABO34167 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO 180.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 295
ID ABR96501 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 296
ID ADA94239 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 297
ID ABR85679 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 298
ID ABR99661 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 299
ID ABM00212 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 300
ID ABM00517 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 301
ID ABO29644 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 302
ID ABM23510 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 303
ID ABM29305 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 304
ID ABO38236 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 305
ID ABO45536 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003073182-A1.
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PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 306
ID ABM20460 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 307
ID ADA81281 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 308
ID ABO16574 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 309
ID ABO18200 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 310
ID ABO22627 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 311
ID ABO22932 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 312
ID ABR92474 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 313
ID ABR81431 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 314
ID ABM77855 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 315
ID ABR89644 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 316
ID ABM26560 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 317
ID ABM13686 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 318
ID ABO28424 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 319
ID ABO30254 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 320
ID ABM07281 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 321
ID ABM03872 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 322
ID ABO37016 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 323
ID ABO41591 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 324
ID ABO35186 standard; protein; 266 AA.
DE Human PRO polypeptide #5.

PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 325
ID ABR25035 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 326
ID ABO47427 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 327
ID ABO47732 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 328
ID ABO48342 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 329
ID ABO51392 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 330
ID ABO51697 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 331
ID ABO50477 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 332
ID ABR79601 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 333
ID ABR16963 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 334
ID ABO17895 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 335
ID ABO20847 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 336
ID ABR96806 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 337
ID ADA38464 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 338
ID ABM12161 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 339
ID ABM16253 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 340
ID ABM24120 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 341
ID ABM14601 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 342
ID ABM04482 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 343
ID ABM06671 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

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PN US2003068730-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
PN US2003032136-A1.
PD 13-FEB-2003.
RESULT 344
ID ABR98111 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 345
ID ABO39151 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 346
ID ABM75416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 347
ID ABM5340 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 348
ID ABM19850 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 349
ID ABO46756 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 350
ID ABO47061 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 351
ID ADA83079 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 352
ID ABR71492 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match
100.0%; Score 1392; DB 6; Length 266;

Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 353
ID ABR72102 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 354
ID ABR98441 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 355
ID ABO6811 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 356
ID ABR84764 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 357
ID ABR73322 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 358
ID ABR76416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 359
ID ABR73017 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 360
ID ABM18083 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 361
ID ABO20542 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 362
ID ABO25285 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
100.0%; Score 1392; DB 6; Length 266;
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Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 363
ID ABO25590 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 364
ID ABR33999 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 365
ID ADA92585 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 366
ID ABR79906 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 367
ID ABM11246 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 368
ID ABO32853 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 369
ID ABO30559 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 370
ID ABO30864 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 371
ID ABM27170 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 372
ID ABM29915 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 373
ID ABM05451 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 374
ID ABM15516 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 375
ID ABM08501 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 376
ID ABO42201 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 377
ID ABO37931 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 378
ID ABO45841 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 379
ID ABM66644 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 380
ID ADB20122 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 381
ID ABM19545 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104552-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 382
ID ABO49257 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 383
ID ABO49562 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 384
ID ADA78374 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 385
ID ABR88119 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 386
ID ADA00333 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO 180.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 387
ID ABM26865 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 388
ID ABM03262 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 389
ID ABO39761 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 390
ID ABO49867 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049776-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 391
ID ABO50782 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 392
ID ABO05238 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 393
ID ABR74542 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 394
ID ABR77021 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 395
ID ABM17778 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 396
ID ABR95829 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 397
ID ABO21762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 398
ID ABO19932 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 399
ID ABO24235 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 400
ID ABR85984 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049759-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 401
ID ABM10636 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 402
ID ABM76635 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 403
ID ABR89339 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 404
ID ABM12466 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 405
ID ABM05756 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 406
ID ABO34881 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 407
ID ABM02957 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 408
ID ABM18935 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 409
ID ABM19240 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 410
ID ABO46451 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 411
ID ABO48952 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 412
ID ABR68995 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 413
ID ABR89034 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 414
ID ABR72407 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 415
ID ABR74237 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 416
ID ABO18505 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 417
ID ABR80211 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 418
ID ABM01432 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 419
ID ABM02042 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003059884-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 420
ID ABR87204 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 421
ID ABM12771 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 422
ID ABM30525 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 423
ID ABM24425 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 424
ID ABO29339 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 425
ID ABO31169 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 426
ID ABM14296 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 427
ID ABM09721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 428
ID ABO38846 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068774-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 429
ID ABM34611 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 430
ID ABO51087 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 431
ID ABO03913 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 432
ID ABO10383 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 433
ID ABO33111 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 434
ID ABR77626 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 435
ID ABR78836 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 436
ID ABO23930 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 437
ID ABR93694 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 438
ID ABO1737 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 439
ID ABM78160 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049764-A1
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 440
ID ABR89949 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 441
ID ADA22146 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO180.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 442
ID ABM27475 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 443
ID ABM13076 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 444
ID ABO31779 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068731-A1
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 445
ID ABM13991 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 446
ID ABM08196 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 447
ID ABO40066 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 448
ID ABM74501 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 449
ID ABM33696 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 450
ID ABM20155 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 451
ID ABO48647 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 452
ID ABO22481 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 453
ID ABR72712 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 454
ID ABO15354 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 455
ID ABR85069 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 456
ID ABO15049 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US20030404919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 457
ID ABO17184 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040077-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 458
ID ABM17473 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044928-A1
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 459
ID ADA06312 standard; protein; 266 AA.
DE Human secreted/transmembrane PRO polypeptide #6.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 460
ID ADA39005 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 461
ID ABR85374 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 462
ID ABM76940 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 463
ID ABO28119 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 464
ID ABM22900 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 465
ID ABM30220 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 466
ID ABM21680 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 467

ID ABM21375 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 468
ID ABM14906 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 469
ID ABO40981 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 470
ID ABO36711 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 471
ID ABO37321 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 472
ID ABM75111 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 473
ID ABM33391 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 474
ID ABO46146 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 475
ID ADA82445 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 476
ID ADB85575 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 477
ID ADB96031 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 478
ID ABM31745 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 479
ID ABM31135 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 480
ID ADB85753 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 481
ID ABM32050 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 482
ID ABM32355 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 483
ID ADB68254 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 484
ID ADB68061 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 485
ID ABM31440 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068761-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 486
ID ABM30830 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 487
ID ADB90878 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 488
ID ADC57503 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 489
ID ADC54867 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 490
ID ADC11734 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 491
ID ADC06958 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 492
ID ADC56156 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 493
ID ADC17137 standard; protein; 266 AA.
DE Mammalian PRO polypeptide (seqID 2).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 494
ID ADC07211 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 495
ID ADC11201 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.

PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 496
ID ADC14835 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 497
ID ADC52330 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 498
ID ADC14323 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 499
ID ADD07855 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 500
ID ADC81680 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 501
ID ADD07322 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 502
ID ADC82213 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 503
ID ADD05483 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 504
ID ADC78249 standard; protein; 266 AA.
DE Human secreted protein SEQ ID NO:56.
PN WO2003072761-A1.
PD 04-SEP-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 505

ID ADD08393 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 506
ID ADD06642 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 507
ID ADC82889 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 508
ID ADD54996 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 509
ID ADD36006 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 510
ID ADD55954 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 511
ID ADD54392 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 512
ID ADE26546 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 513
ID ADE26013 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 514
ID ADF66950 standard; protein; 266 AA.
DE Human PRO180 amino acid sequence SEQ ID NO:23.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;

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RESULT 515
ID ADG01007 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003078387-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 516
ID ADG08560 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 517
ID ADG02478 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 518
ID ADG01185 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 519
ID ADF95360 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 520
ID ADF95181 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 521
ID ADG12175 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 522
ID ADH24034 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 523
ID ADH34060 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 524
ID ADH24204 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 525
ID ADH23864 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 526
ID ADH08835 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 527
ID ADG85268 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 528
ID ADH24544 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 529
ID ADH37400 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 530
ID ADH01989 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 531
ID ADH37570 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 532
ID ADG85608 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 533
ID ADH24204 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
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PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 534
ID ADH38498 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 535
ID ADG83619 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 536
ID ADH29427 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 537
ID ADH27543 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 538
ID ADH37740 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 539
ID ADH37917 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 540
ID ADH57337 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 541
ID ADH53479 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 542
ID ADH53649 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181641-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 543
ID ADH51985 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 544
ID ADH49840 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 545
ID ADI25350 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 546
ID ADH90143 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 547
ID ADI25520 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 548
ID ADH97694 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 549
ID ADI35204 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 550
ID ADI03542 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 551
ID ADI11899 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 552
ID ADH9973 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 553
ID ADH9966 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003049682-A1.
PD 13-WAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 7; Length 266;
RESULT 554
ID ADH98374 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 555
ID ADI1049 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 556
ID ADI11559 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 557
ID ADH98204 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 558
ID ADH98544 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 559
ID ADH98034 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 560
ID ADI05022 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;

RESULT 561
ID ADI03372 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 562
ID ADI04767 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 563
ID ADH78221 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 564
ID ADI19565 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 565
ID ADH90313 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 566
ID ADI03032 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 567
ID ADH77881 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 568
ID ADH97864 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 569
ID ADI01249 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 570
ID ADI01249 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;

ID ADI01944 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 571
ID ADI03202 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 572
ID ADI11389 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 573
ID ADI02291 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 574
ID ADI11729 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 575
ID ADI05366 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 576
ID ADH79438 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 577
ID ADI19395 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 578
ID ADI05196 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 579
ID ADH79608 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 580
ID ADI01434 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 581
ID ADI01604 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 582
ID ADI01774 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 583
ID ADH79778 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 584
ID ADI04596 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 585
ID ADI02732 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 586
ID ADH78051 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 587
ID ADI25690 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 588
ID ADI25860 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 589
ID ADK65372 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 590
ID ADH98714 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 591
ID ADH79955 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 592
ID ADL32616 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 593
ID ADM30150 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 594
ID ADL33686 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 595
ID ADC52140 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 596
ID ADE74147 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 597
ID ADE74759 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003211574-A1.
PD 13-NOV-2003.

Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 598
ID ADF35149 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 599
ID ADG11399 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 600
ID ADF95972 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 601
ID ADG04243 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 602
ID ADG00403 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 603
ID ADH06572 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 604
ID ADH06402 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 605
ID ADG68823 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 606
ID ADH27713 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 607

ID ADH25054 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 608
ID ADH33686 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 609
ID ADG82659 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 610
ID ADH02329 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 611
ID ADH07936 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 612
ID ADG69333 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 613
ID ADH39154 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 614
ID ADH25940 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 615
ID ADG3894 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 616
ID ADH19269 standard; protein; 266 AA.

DE Human secreted/transmembrane protein PRO180.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 617
ID ADG85438 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 618
ID ADH06232 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 619
ID ADH30063 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 620
ID ADH24374 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 621
ID ADH32909 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 622
ID ADG69503 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 623
ID ADH07766 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 624
ID ADG85778 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 625
ID ADH39324 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 626
ID ADH33516 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 627
ID ADH33856 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 628
ID ADH01066 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 629
ID ADG69673 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 630
ID ADH20762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 631
ID ADH02159 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 632
ID ADG69163 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 633
ID ADG85948 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 634
ID ADH24884 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180909-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 635
ID ADH39501 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 636
ID ADH19802 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 637
ID ADH02499 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 638
ID ADG68993 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 639
ID ADH07596 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 640
ID ADG86118 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 641
ID ADH24714 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 642
ID ADH25762 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 643
ID ADH38328 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 644
 ID ADH57167 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181642-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 645
 ID ADH52155 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180921-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 646
 ID ADH49521 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003180857-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 647
 ID ADH90483 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181700-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 648
 ID ADH90483 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003181683-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 649
 ID ADH98884 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003190698-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 650
 ID ADI02114 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003190699-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 651
 ID ADH90653 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181701-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 652
 ID ADJ54648 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2004023321-A1.
 PD 05-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;

Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 653
 ID ADJ98528 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003187197-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 654
 ID ADJ98698 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003187228-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 655
 ID ADH78857 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181703-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 656
 ID ADJ99091 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003186408-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 657
 ID ADJ99261 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003187196-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 658
 ID ADJ98879 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003187242-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 659
 ID ADH79027 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003181702-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 660
 ID ADK00887 standard; protein; 266 AA.
 DE Human PRO polypeptide #1.
 PN US2003186407-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 661
 ID ADK14408 standard; protein; 266 AA.
 DE Novel human secreted and transmembrane protein PRO180.
 PN US2003187229-A1.
 PD 02-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;
 Best Local Similarity 100.0%; Pred. No. 4.7e-149;
 RESULT 662
 ID ADJ54648 standard; protein; 266 AA.
 DE Human PRO polypeptide #5.
 PN US2004023321-A1.
 PD 05-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1392; DB 8; Length 266;

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RESULT 662
ID  ADJ44419 standard; protein; 266 AA.
DE  Human PRO polypeptide #5.
PN  US2004038337-A1.
PD  26-FEB-2004.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%; Score 1392; DB 8; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 663
ID  ADM31315 standard; protein; 266 AA.
DE  Novel human secreted and transmembrane protein PRO180.
PN  US2004048334-A1.
PD  11-MAR-2004.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%; Score 1392; DB 8; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 664
ID  ADM36362 standard; protein; 266 AA.
DE  Novel human secreted and transmembrane protein PRO180.
PN  US2004053358-A1.
PD  18-MAR-2004.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%; Score 1392; DB 8; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 665
ID  ADM40167 standard; protein; 266 AA.
DE  Novel human secreted and transmembrane protein PRO180.
PN  US2004048335-A1.
PD  11-MAR-2004.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%; Score 1392; DB 8; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 666
ID  ADM80857 standard; protein; 266 AA.
DE  Human PRO polypeptide #1.
PN  US2004058411-A1.
PD  25-MAR-2004.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%; Score 1392; DB 8; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 667
ID  ADN60677 standard; protein; 266 AA.
DE  Human secreted polypeptide #9.
PN  US2004038277-A1.
PD  26-FEB-2004.
PA  (HUMA-) HUMAN GENOME SCI INC.
    Query Match      100.0%; Score 1392; DB 8; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 668
ID  ADN37775 standard; protein; 266 AA.
DE  Novel human secreted and transmembrane protein PRO180.
PN  US2004091959-A1.
PD  13-MAY-2004.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%; Score 1392; DB 8; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 669
ID  ADY77697 standard; protein; 266 AA.
DE  Neoplastic disease detection protein PRO180.
PN  US2005059102-A1.
PD  17-MAR-2005.
PA  (EATO/) EATON D L.
PA  (FILV/) FILVAROFF E.
PA  (GERR/) GERRITSEN M E.
PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GRIM/) GRIMALDI J C.
PA  (GURN/) GURNEY A L.
PA  (WATA/) WATANABE C K.
PA  (WOOD/) WOOD W I.
    Query Match      100.0%; Score 1392; DB 9; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 670
ID  ADJ46037 standard; protein; 267 AA.
DE  Novel human secreted protein-related protein sequence SeqID190.
PN  US2003144490-A1.
ID  AEA38350 standard; protein; 266 AA.
DE  Human secreted/transmembrane protein cDNA, #73.
PN  US2005112725-A1.
PD  26-MAY-2005.
PA  (GETH ) GENENTECH INC.
    Query Match      100.0%; Score 1392; DB 9; Length 266;
    Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 671
ID  AAY27575 standard; protein; 267 AA.
DE  Human secreted protein encoded by gene No. 9.
PN  WO9924836-A1.
PD  20-MAY-1999.
PA  (HUMA-) HUMAN GENOME SCI INC.
    Query Match      100.0%; Score 1392; DB 2; Length 267;
    Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 672
ID  ADG78386 standard; protein; 267 AA.
DE  Human secreted protein #9.
PN  US2003211472-A1.
PD  13-NOV-2003.
PA  (FENG/) FENG P.
PA  (RUBE/) RUBEN S M.
PA  (ROSE/) ROSEN C A.
PA  (EBNE/) EBNER R.
PA  (OLSE/) OLSEN H S.
PA  (NIJ/) NI J.
PA  (WEI/) WEI Y.
PA  (SOPP/) SOPPET D R.
PA  (MOOR/) MOORE P A.
PA  (KYAW/) KYAW H.
PA  (LAE/) LAPLEUR D W.
PA  (SHI/) SHI Y.
PA  (JANA/) JANAT F.
PA  (ENDR/) ENDRESS G A.
PA  (CART/) CARTER K C.
    Query Match      100.0%; Score 1392; DB 8; Length 267;
    Best Local Similarity 100.0%; Pred. No. 4.7e-149;
RESULT 673
ID  ABB12041 standard; peptide; 275 AA.
DE  Human secreted protein homologue, SEQ ID NO:2411.
PN  WO200157188-A2.
PD  09-AUG-2001.
PA  (HYSE-) HYSEQ INC.
    Query Match      100.0%; Score 1392; DB 4; Length 275;
    Best Local Similarity 100.0%; Pred. No. 4.9e-149;
RESULT 674
ID  AAM41354 standard; protein; 275 AA.
DE  Human polypeptide SEQ ID NO 6285.
PN  WO20015312-A1.
PD  26-JUL-2001.
PA  (HYSE-) HYSEQ INC.
    Query Match      100.0%; Score 1392; DB 4; Length 275;
    Best Local Similarity 100.0%; Pred. No. 4.9e-149;
RESULT 675
ID  AAB87526 standard; protein; 266 AA.
DE  Human PRO180.
PN  WO200116318-A2.
PD  08-MAR-2001.
PA  (GETH ) GENENTECH INC.
    Query Match      99.9%; Score 1390; DB 4; Length 266;
    Best Local Similarity 99.6%; Pred. No. 8e-149;
RESULT 676
ID  AAY36185 standard; protein; 267 AA.
DE  Human secreted protein #57.
PN  WO9925825-A2.
PD  27-MAY-1999.
PA  (GEST) GENSET.
    Query Match      99.7%; Score 1388; DB 2; Length 267;
    Best Local Similarity 99.6%; Pred. No. 1.3e-148;
RESULT 677
ID  ADJ46037 standard; protein; 267 AA.
DE  Novel human secreted protein-related protein sequence SeqID190.
PN  US2003144490-A1.
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PD 31-JUL-2003.
ID (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUERET L.
Query Match 99.7%; Score 1388; DB 7; Length 267;
Best Local Similarity 99.8%; Pred. No. 1.3e-148;
RESULT 678
ID ADP19446 standard; protein; 267 AA.
DE Human secreted polypeptide #297.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 99.7%; Score 1388; DB 8; Length 267;
Best Local Similarity 99.8%; Pred. No. 1.3e-148;
RESULT 679
ID AAY29866 standard; protein; 208 AA.
DE Human secreted protein clone pe318_4.
PN WO9946287-A1.
PD 16-SEP-1999.
PA (GEMY) GENETICS INST INC.
Query Match 77.4%; Score 1078; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
RESULT 680
ID ABP75476 standard; protein; 166 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 660.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 58.6%; Score 816; DB 6; Length 166;
Best Local Similarity 93.4%; Pred. No. 6.5e-84;
RESULT 681
ID AAB88330 standard; protein; 136 AA.
DE Human membrane or secretory protein clone PSEC0031.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 52.1%; Score 725; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.1e-73;
RESULT 682
ID ADY63025 standard; protein; 136 AA.
DE Human clone PSEC0031 protein, SEQ ID 28.
PN EP1514933-A1.
PD 16-MAR-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 52.1%; Score 725; DB 9; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.1e-73;
RESULT 683
ID AAY36138 standard; protein; 172 AA.
DE Human secreted protein #10.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 42.8%; Score 595.5; DB 2; Length 172;
Best Local Similarity 79.4%; Pred. No. 7.6e-59;
RESULT 684
ID ADJ45943 standard; protein; 172 AA.
DE Novel human secreted protein-related protein sequence SeqID96.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUERET L.
Query Match 42.8%; Score 595.5; DB 7; Length 172;
Best Local Similarity 79.4%; Pred. No. 7.6e-59;
RESULT 685
ID ADM04182 standard; protein; 238 AA.
DE Human protein of the invention SEQ ID NO:2867.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 34.9%; Score 486.5; DB 7; Length 238;
Best Local Similarity 38.6%; Pred. No. 2.8e-46;
RESULT 686

ID AAE26425 standard; protein; 231 AA.
DE Human transmembrane protein (TMP)-11 protein.
PN WO200234783-A2.
PD 02-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 34.5%; Score 480.5; DB 5; Length 231;
Best Local Similarity 38.7%; Pred. No. 1.3e-45;
RESULT 687
ID ADK70499 standard; protein; 231 AA.
DE Respiratory disease differentially expressed protein #65.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 34.5%; Score 480.5; DB 8; Length 231;
Best Local Similarity 38.7%; Pred. No. 1.3e-45;
RESULT 688
ID AAE05342 standard; protein; 238 AA.
DE Mouse secreted protein #1.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 34.4%; Score 479.5; DB 4; Length 238;
Best Local Similarity 37.3%; Pred. No. 1.8e-45;
RESULT 689
ID ABO00865 standard; protein; 246 AA.
DE Polypeptide encoded by novel human contig #116.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 33.2%; Score 461.5; DB 6; Length 246;
Best Local Similarity 39.3%; Pred. No. 2.1e-43;
RESULT 690
ID ABB60356 standard; protein; 246 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7860.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 26.0%; Score 361.5; DB 4; Length 246;
Best Local Similarity 33.6%; Pred. No. 4.7e-32;
RESULT 691
ID AAY36219 standard; protein; 69 AA.
DE Human secreted protein #91.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 25.7%; Score 358; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 2e-32;
RESULT 692
ID AAY36172 standard; protein; 69 AA.
DE Human secreted protein #44.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 25.7%; Score 358; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 2e-32;
RESULT 693
ID ADJ46071 standard; protein; 69 AA.
DE Novel human secreted protein-related protein sequence SeqID224.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUERET L.
Query Match 25.7%; Score 358; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 2e-32;
RESULT 694
ID ADJ45977 standard; protein; 69 AA.
DE Novel human secreted protein-related protein sequence SeqID130.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUERET L.

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Query Match      25.7%; Score 358; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 2e-32;
RESULT 695
ID ADP19480 standard; protein; 69 AA.
DE Human secreted polypeptide #331.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST ) GENSET SA.
Query Match      25.7%; Score 358; DB 8; Length 69;
Best Local Similarity 100.0%; Pred. No. 2e-32;
RESULT 696
ID ABG28122 standard; protein; 200 AA.
DE Novel human diagnostic protein #28113.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match      25.6%; Score 356.5; DB 4; Length 200;
Best Local Similarity 74.0%; Pred. No. 1.3e-31;
RESULT 697
ID ABB97776 standard; protein; 85 AA.
DE Human secretory polypeptide (SPTM) 28.
PN WO20020756-A2.
PD 14-MAR-2002.
PA (INCV-) INCYTE GENOMICS INC.
Query Match      25.6%; Score 356; DB 5; Length 85;
Best Local Similarity 86.1%; Pred. No. 4.6e-32;
RESULT 698
ID AAY04148 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO:19.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST ) GENSET.
Query Match      25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 9.8e-32;
RESULT 699
ID AAU931616 standard; protein; 69 AA.
DE Human 5' EST secreted protein clone 58-34-2-E7-FL2.
PN WO9906551-A2.
PD 11-FEB-1999.
PA (GEST ) GENSET.
Query Match      25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 9.8e-32;
RESULT 700
ID AAY04166 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO:19.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST ) GENSET.
Query Match      25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 9.8e-32;
RESULT 701
ID AAY35882 standard; protein; 69 AA.
DE Extended human secreted protein sequence, SEQ ID NO. 19.
PN WO991236-A2.
PD 24-JUN-1999.
PA (GEST ) GENSET.
Query Match      25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 9.8e-32;
RESULT 702
ID AAY59645 standard; protein; 69 AA.
DE Secreted protein extended EST protein sequence #2.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST ) GENSET.
Query Match      25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 9.8e-32;
RESULT 703
ID AAY01590 standard; protein; 69 AA.
DE Secreted protein encoded by an extended 5' EST cDNA sequence.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST ) GENSET.
Query Match      25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 9.8e-32;
RESULT 704
ID AAY12982 standard; protein; 69 AA.
DE Human secreted protein encoded by 5' EST clone 58-34-2-E7-FL2.
PN WO9906552-A2.
PD 11-FEB-1999.
PA (GEST ) GENSET.
Query Match      25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 9.8e-32;
RESULT 705
ID AAY25451 standard; protein; 69 AA.
DE Human secreted protein 2 derived from extended cDNA.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST ) GENSET.
Query Match      25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 9.8e-32;
RESULT 706
ID AAY12672 standard; peptide; 69 AA.
DE Human 5' EST secreted protein.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST ) GENSET.
Query Match      25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 9.8e-32;
RESULT 707
ID AAG00010 standard; protein; 69 AA.
DE Human secreted protein #1.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST ) GENSET.
Query Match      25.3%; Score 352; DB 3; Length 69;
Best Local Similarity 98.5%; Pred. No. 9.8e-32;
RESULT 708
ID ADU73027 standard; protein; 69 AA.
DE cDNA 58-34-2-E7-FL2-encoded secreted protein, SEQ ID NO:1.
PN US6822072-B1.
PD 23-NOV-2004.
PA (GEST ) GENSET SA.
Query Match      25.3%; Score 352; DB 8; Length 69;
Best Local Similarity 98.5%; Pred. No. 9.8e-32;
RESULT 709
ID ABB89768 standard; protein; 180 AA.
DE Human polypeptide SEQ ID NO 2144.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      22.8%; Score 317.5; DB 5; Length 180;
Best Local Similarity 33.3%; Pred. No. 3e-27;
RESULT 710
ID AAG81279 standard; protein; 114 AA.
DE Human AFP protein sequence SEQ ID NO:76.
PN WO200129221-A2.
PD 26-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match      19.6%; Score 272.5; DB 4; Length 114;
Best Local Similarity 47.5%; Pred. No. 2.1e-22;
RESULT 711
ID AAB93632 standard; protein; 132 AA.
DE Human protein sequence SEQ ID NO:13115.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match      18.0%; Score 251; DB 4; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.1e-20;
RESULT 712
ID ADL06520 standard; protein; 132 AA.
DE Human tumour-associated antigenic target (TAT) polypeptide #19.
PN WO2004016225-A2.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match      18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.1e-20;
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RESULT 713
ID ADJ75472 standard; protein; 132 AA.
DE Marker gene related amino acid sequence SEQ ID NO:724.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.1e-20;
RESULT 714
ID ADRI14452 standard; protein; 132 AA.
DE Human NF-kappaB pathway-associated protein SeqID453.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.1e-20;
RESULT 715
ID ADP24981 standard; protein; 132 AA.
DE PKO polypeptide SEQ ID NO:2159.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.1e-20;
RESULT 716
ID ADU06610 standard; protein; 132 AA.
DE Novel bronchial cancer-associated human protein SeqID836.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 7.1e-20;
RESULT 717
ID ADS11008 standard; protein; 233 AA.
DE Human therapeutic protein - SEQ ID 1245.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 15.8%; Score 220.5; DB 8; Length 233;
Best Local Similarity 27.2%; Pred. No. 4.5e-16;
RESULT 718
ID ABO00507 standard; protein; 283 AA.
DE Novel human polypeptide #94.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 15.4%; Score 214.5; DB 6; Length 283;
Best Local Similarity 26.2%; Pred. No. 2.8e-15;
RESULT 719
ID AAB08866 standard; protein; 249 AA.
DE Amino acid sequence of a human secretory protein.
PN WO200052151-A2.
PD 08-SEP-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 15.2%; Score 212; DB 3; Length 249;
Best Local Similarity 26.5%; Pred. No. 4.6e-15;
RESULT 720
ID AAM38964 standard; protein; 249 AA.
DE Human polypeptide SEQ ID NO 2109.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.2%; Score 212; DB 4; Length 249;
Best Local Similarity 26.5%; Pred. No. 4.6e-15;
RESULT 721
ID AAM51628 standard; protein; 249 AA.
DE Human plasminogen activator inhibitor 2-27 polypeptide.
PN CN1313331-A.
PD 19-SEP-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 15.2%; Score 212; DB 5; Length 249;
Best Local Similarity 24.5%; Pred. No. 3.6e-09;

Best Local Similarity 26.5%; Pred. No. 4.6e-15;
RESULT 722
ID ADP18677 standard; protein; 249 AA.
DE Human protein encoded by TA7414 CDNA used to treat cancer SeqID 37.
PN WO2004045516-A2.
PD 03-JUN-2004.
PA (GETH) GENENTECH INC.
Query Match 15.2%; Score 212; DB 8; Length 249;
Best Local Similarity 26.5%; Pred. No. 4.6e-15;
RESULT 723
ID RAY12179 standard; protein; 36 AA.
DE Human 5' EST secreted protein SEQ ID NO: 492.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 14.0%; Score 195; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.7e-14;
RESULT 724
ID AAM40750 standard; protein; 274 AA.
DE Human polypeptide SEQ ID NO 5681.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 192.5; DB 4; Length 274;
Best Local Similarity 31.4%; Pred. No. 8.5e-13;
RESULT 725
ID ABG17213 standard; protein; 308 AA.
DE Novel human diagnostic protein #17204.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 180; DB 4; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
RESULT 726
ID ABG16460 standard; protein; 466 AA.
DE Novel human diagnostic protein #16451.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.7%; Score 176.5; DB 4; Length 466;
Best Local Similarity 60.0%; Pred. No. 1.2e-10;
RESULT 727
ID AAE00332 standard; protein; 253 AA.
DE Human membrane-bound protein-60 alternative mature protein sequence.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 11.5%; Score 160.5; DB 4; Length 253;
Best Local Similarity 24.5%; Pred. No. 3.3e-09;
RESULT 728
ID AAE00331 standard; protein; 256 AA.
DE Human membrane-bound protein-60 (Zsig60) mature protein sequence.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 11.5%; Score 160.5; DB 4; Length 256;
Best Local Similarity 24.5%; Pred. No. 3.3e-09;
RESULT 729
ID AAB18985 standard; protein; 271 AA.
DE Amino acid sequence of a human transmembrane protein.
PN WO200056891-A2.
PD 28-SEP-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 11.5%; Score 160.5; DB 3; Length 271;
Best Local Similarity 24.5%; Pred. No. 3.6e-09;
RESULT 730
ID AAE00330 standard; protein; 271 AA.
DE Human membrane-bound protein-60 (Zsig60).
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 11.5%; Score 160.5; DB 4; Length 271;
Best Local Similarity 24.5%; Pred. No. 3.6e-09;

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RESULT 731
ID AAY48244 standard; protein; 304 AA.
DE Human prostate cancer-associated protein 30.
PN DE19811193-A1.
PA (META-) METAGEN GFS GENOMFORSCHUNG MBH.
Query Match 10.9%; Score 152; DB 2; Length 304;
Best Local Similarity 24.0%; Pred. No. 3.9e-08;
RESULT 732
ID AAE00334 standard; protein; 160 AA.
DE Human membrane-bound protein-60 alternative mature extracellular portion.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.9%; Score 151.5; DB 4; Length 160;
Best Local Similarity 29.5%; Pred. No. 1.8e-08;
RESULT 733
ID AAE00333 standard; protein; 163 AA.
DE Human membrane-bound protein-60 (Zsig60) mature extracellular portion.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.9%; Score 151.5; DB 4; Length 163;
Best Local Similarity 29.5%; Pred. No. 1.9e-08;
RESULT 734
ID AAY94930 standard; protein; 437 AA.
DE Human secreted protein clone qal36_1 protein sequence SEQ ID NO:66.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEM) GENETICS INST INC.
Query Match 10.9%; Score 151.5; DB 3; Length 437;
Best Local Similarity 26.8%; Pred. No. 7.4e-08;
RESULT 735
ID AAY95013 standard; protein; 178 AA.
DE Human secreted protein vc48_1, SEQ ID NO:66.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 10.6%; Score 147.5; DB 3; Length 178;
Best Local Similarity 24.9%; Pred. No. 6.1e-08;
RESULT 736
ID ADN02727 standard; protein; 255 AA.
DE Human receptor and membrane -associated protein #30.
PN WO2004029218-A2.
PD 08-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.5%; Score 146.5; DB 8; Length 255;
Best Local Similarity 24.6%; Pred. No. 1.3e-07;
RESULT 737
ID ABO00615 standard; protein; 63 AA.
DE Novel human polypeptide #202.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 9.1%; Score 126; DB 6; Length 63;
Best Local Similarity 47.2%; Pred. No. 4e-06;
RESULT 738
ID ADS11007 standard; protein; 127 AA.
DE Human therapeutic protein - SEQ ID 1244.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 8.8%; Score 122.5; DB 8; Length 127;
Best Local Similarity 32.1%; Pred. No. 2.6e-05;
RESULT 739
ID AAY04149 standard; peptide; 21 AA.
DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.
PN WO906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 740
ID AAO20328 standard; peptide; 21 AA.
DE Human 5' EST secreted protein SEQ ID NO:20.
PN WO906551-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 741
ID AAY12516 standard; peptide; 21 AA.
DE Human 5' EST signal peptide SEQ ID NO: 20 from WO 9906553.
PN WO9906553-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 742
ID AAY35883 standard; peptide; 21 AA.
DE Signal peptide of extended secreted protein, SEQ ID NO. 20.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 743
ID AAY59644 standard; peptide; 21 AA.
DE Secreted protein extended EST signal peptide #2.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 744
ID AAY25452 standard; peptide; 21 AA.
DE Human secreted protein 2 signal peptide derived from extended cdna.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 745
ID AAY12671 standard; peptide; 21 AA.
DE Human 5' EST secreted protein signal peptide.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 746
ID AAY11711 standard; protein; 21 AA.
DE Peptide encoded by extended cdna derived from 5' EST.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 747
ID AAY64644 standard; peptide; 21 AA.
DE Human 58-34-2-E7-FL2 signal peptide.
PN WO9953051-A2.
PD 21-OCT-1999.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 748
ID AAG00011 standard; peptide; 21 AA.
DE Human secreted protein #1 signal peptide.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 749
ID AAO20328 standard; peptide; 21 AA.
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DE Signal peptide encoded by the cDNA 58-34-2-E7-FL2.
PN CA2343602-A1.
PD 18-OCT-2001.
PA (GEST) GENSET.
Query Match 8.5%; Score 118; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 750
ID ADJ45867 standard; peptide; 21 AA.
DE Novel human secreted protein-related peptide sequence SeqID20.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDMA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 8.5%; Score 118; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 751
ID ADM77739 standard; peptide; 21 AA.
DE Signal sequence #2.
PN US2003162176-A1.
PD 28-AUG-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 8.5%; Score 118; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 752
ID ADU71405 standard; peptide; 21 AA.
DE cDNA 58-34-2-E7-FL2-encoded secretory signal peptide, SEQ ID NO:2.
PN US6822072-B1.
PD 23-NOV-2004.
PA (GEST) GENSET SA.
Query Match 8.5%; Score 118; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 753
ID ADZ89199 standard; peptide; 21 AA.
DE Signal peptide from secreted protein encoded by extended EST cDNA #2.
PN US2005106599-A1.
PD 19-MAY-2005.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 8.5%; Score 118; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 754
ID ADZ72396 standard; peptide; 21 AA.
DE Human 5' EST encoded signal peptide SEQ ID NO:2.
PN US2005106595-A1.
PD 19-MAY-2005.
PA (GEST) GENSET SA.
Query Match 8.5%; Score 118; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
RESULT 755
ID AAY04167 standard; peptide; 21 AA.
DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.
PN WO906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 8.1%; Score 113; DB 2; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e-05;
RESULT 756
ID AAU04087 standard; peptide; 21 AA.
DE Signal peptide encoded by Human cDNA 58-34-2-E7-FL2.
PN EP1104808-A1.
PD 06-JUN-2001.
PA (GEST) GENSET.
Query Match 8.1%; Score 113; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
RESULT 757
ID ABB60233 standard; protein; 275 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7491.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 7.7%; Score 106.5; DB 4; Length 275;
Best Local Similarity 21.3%; Pred. No. 0.005;
RESULT 758
ID AAB38499 standard; peptide; 220 AA.
DE Fragment of human secreted protein encoded by gene 53 clone HPABG18.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.5%; Score 105; DB 3; Length 220;
Best Local Similarity 22.8%; Pred. No. 0.0055;
RESULT 759
ID AAM93195 standard; protein; 218 AA.
DE Human polypeptide, SEQ ID NO: 2575.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 7.3%; Score 101; DB 4; Length 218;
Best Local Similarity 22.8%; Pred. No. 0.015;
RESULT 760
ID ADL30542 standard; protein; 218 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2575.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.3%; Score 101; DB 8; Length 218;
Best Local Similarity 22.8%; Pred. No. 0.015;
RESULT 761
ID AEB39816 standard; protein; 581 AA.
DE L. pneumophila protein SEQ ID NO 3148.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON I BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 7.1%; Score 99.5; DB 9; Length 581;
Best Local Similarity 24.4%; Pred. No. 0.088;
RESULT 762
ID ADM06102 standard; protein; 187 AA.
DE Human protein of the invention SEQ ID NO:4787.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.1%; Score 99; DB 7; Length 187;
Best Local Similarity 23.4%; Pred. No. 0.021;
RESULT 763
ID ABU45347 standard; protein; 1066 AA.
DE Protein encoded by Prokaryotic essential gene #30874.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1066;
Best Local Similarity 19.5%; Pred. No. 0.26;
RESULT 764
ID ABU47563 standard; protein; 1120 AA.
DE Protein encoded by Prokaryotic essential gene #33090.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1120;
Best Local Similarity 19.5%; Pred. No. 0.28;
RESULT 765
ID ABU46980 standard; protein; 1120 AA.
DE Protein encoded by Prokaryotic essential gene #32507.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1120;
Best Local Similarity 19.5%; Pred. No. 0.28;
RESULT 766
ID AEB42187 standard; protein; 268 AA.
DE L. pneumophila protein SEQ ID NO 6519.

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PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP ) INST PASTEUR.
PA (INRM ) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
  Query Match      6.8%; Score 94.5; DB 9; Length 268;
  Best Local Similarity 22.8%; Pred. No. 0.11;
RESULT 767
ID ABB39048 standard; protein; 291 AA.
DE L. pneumophila protein SEQ ID NO 3380.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP ) INST PASTEUR.
PA (INRM ) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
  Query Match      6.8%; Score 94.5; DB 9; Length 291;
  Best Local Similarity 22.6%; Pred. No. 0.13;
RESULT 768
ID ABB39048 standard; protein; 291 AA.
DE L. pneumophila protein SEQ ID NO 3380.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP ) INST PASTEUR.
PA (INRM ) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
  Query Match      6.8%; Score 94.5; DB 9; Length 291;
  Best Local Similarity 22.6%; Pred. No. 0.13;
RESULT 769
ID ABB39048 standard; protein; 291 AA.
DE L. pneumophila protein SEQ ID NO 3380.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP ) INST PASTEUR.
PA (INRM ) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
  Query Match      6.8%; Score 94.5; DB 9; Length 291;
  Best Local Similarity 22.6%; Pred. No. 0.13;
RESULT 770
ID ABB39048 standard; protein; 291 AA.
DE L. pneumophila protein SEQ ID NO 3380.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP ) INST PASTEUR.
PA (INRM ) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
  Query Match      6.8%; Score 94.5; DB 9; Length 291;
  Best Local Similarity 22.6%; Pred. No. 0.13;
RESULT 771
ID ABB39048 standard; protein; 291 AA.
DE L. pneumophila protein SEQ ID NO 3380.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP ) INST PASTEUR.
PA (INRM ) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
  Query Match      6.8%; Score 94.5; DB 9; Length 291;
  Best Local Similarity 22.6%; Pred. No. 0.13;
RESULT 772
ID ABB39048 standard; protein; 291 AA.
DE L. pneumophila protein SEQ ID NO 3380.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP ) INST PASTEUR.
PA (INRM ) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
  Query Match      6.8%; Score 94.5; DB 9; Length 291;
  Best Local Similarity 22.6%; Pred. No. 0.13;
RESULT 773
ID ABB39048 standard; protein; 291 AA.
DE L. pneumophila protein SEQ ID NO 3380.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP ) INST PASTEUR.
PA (INRM ) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
  Query Match      6.8%; Score 94.5; DB 9; Length 291;
  Best Local Similarity 22.6%; Pred. No. 0.13;
RESULT 774
ID ABB39048 standard; protein; 291 AA.
DE L. pneumophila protein SEQ ID NO 3380.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP ) INST PASTEUR.
PA (INRM ) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
  Query Match      6.8%; Score 94.5; DB 9; Length 291;
  Best Local Similarity 22.6%; Pred. No. 0.13;
RESULT 775
ID ADC94520 standard; protein; 291 AA.
DE E. faecium protein sequence SEQ ID 4147.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
  Query Match      6.6%; Score 91.5; DB 7; Length 291;
  Best Local Similarity 22.9%; Pred. No. 0.27;
RESULT 776
ID ADN23444 standard; protein; 373 AA.
DE Bacterial polypeptide #6097.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
  Query Match      6.6%; Score 91.5; DB 8; Length 373;
  Best Local Similarity 23.0%; Pred. No. 0.39;
RESULT 777
ID AAU03808 standard; protein; 387 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #7.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA ) PHARMACIA & UPJOHN.
  Query Match      6.6%; Score 91.5; DB 4; Length 387;
  Best Local Similarity 23.0%; Pred. No. 0.41;
RESULT 778
ID ABB91939 standard; protein; 712 AA.
DE Herbicidally active polypeptide SEQ ID NO 1150.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB ) BAYER AG.
  Query Match      6.6%; Score 91.5; DB 5; Length 712;
  Best Local Similarity 22.2%; Pred. No. 0.94;
RESULT 779
ID ADX68404 standard; protein; 486 AA.
DE Plant full length insert polypeptide seqid 39247.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
  Query Match      6.5%; Score 91; DB 8; Length 486;
  Best Local Similarity 22.6%; Pred. No. 0.63;
RESULT 780
ID ADX87645 standard; protein; 486 AA.
DE Plant full length insert polypeptide seqid 50309.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
  Query Match      6.5%; Score 91; DB 8; Length 486;
  Best Local Similarity 22.6%; Pred. No. 0.63;
RESULT 781
ID ADY12322 standard; protein; 487 AA.
DE Plant full length insert polypeptide seqid 68137.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
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Query Match 6.5%; Score 91; DB 8; Length 487;
Best Local Similarity 22.6%; Pred. No. 0.63;
RESULT 782
ID ADN46339 standard; protein; 451 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID217.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.5%; Score 90.5; DB 8; Length 451;
Best Local Similarity 21.2%; Pred. No. 0.65;
RESULT 783
ID AAB76803 standard; protein; 283 AA.
DE Corynebacterium glutamicum MCT protein SEQ ID NO:588.
PN WO200100805-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 6.5%; Score 90; DB 4; Length 283;
Best Local Similarity 23.8%; Pred. No. 0.39;
RESULT 784
ID AAG89779 standard; protein; 283 AA.
DE C glutamicum protein fragment SEQ ID NO: 3533.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.5%; Score 90; DB 4; Length 283;
Best Local Similarity 23.8%; Pred. No. 0.39;
RESULT 785
ID ADP98865 standard; protein; 505 AA.
DE C. albicans specific gene, orf6.4442, protein sequence.
PN WO2004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 90; DB 8; Length 505;
Best Local Similarity 20.5%; Pred. No. 0.87;
RESULT 786
ID ABU4537 standard; protein; 458 AA.
DE Protein encoded by Prokaryotic essential gene #31064.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 89.5; DB 6; Length 458;
Best Local Similarity 22.8%; Pred. No. 0.86;
RESULT 787
ID ABP26393 standard; protein; 579 AA.
DE Streptococcus polypeptide SEQ ID NO 1962.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.4%; Score 89.5; DB 5; Length 579;
Best Local Similarity 24.8%; Pred. No. 1.2;
RESULT 788
ID ADV88815 standard; protein; 579 AA.
DE Streptococcus agalactiae protein sequence, SEQ ID 1209.
PN FR2824074-A1.
PD 31-OCT-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.4%; Score 89.5; DB 8; Length 579;
Best Local Similarity 24.8%; Pred. No. 1.2;
RESULT 789
ID ADV82204 standard; protein; 579 AA.
DE Streptococcus agalactiae protein, SEQ ID 3345.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.4%; Score 89.5; DB 8; Length 579;
Best Local Similarity 24.8%; Pred. No. 1.2;
RESULT 790
ID ADV80068 standard; protein; 579 AA.
DE Streptococcus agalactiae protein, SEQ ID 1209.

PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.4%; Score 89.5; DB 8; Length 579;
Best Local Similarity 24.8%; Pred. No. 1.2;
RESULT 791
ID ABU50406 standard; protein; 428 AA.
DE Protein encoded by Prokaryotic essential gene #35933.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 89; DB 6; Length 428;
Best Local Similarity 21.6%; Pred. No. 0.9;
RESULT 792
ID AAB94689 standard; protein; 637 AA.
DE Human protein sequence SEQ ID NO:15654.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.4%; Score 89; DB 4; Length 637;
Best Local Similarity 21.5%; Pred. No. 1.6;
RESULT 793
ID ABU23408 standard; protein; 642 AA.
DE Protein encoded by Prokaryotic essential gene #8935.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 89; DB 6; Length 642;
Best Local Similarity 20.8%; Pred. No. 1.6;
RESULT 794
ID AAU03497 standard; protein; 757 AA.
DE Human sterol sensing domain protein.
PN WO200146227-A2.
PD 28-JUN-2001.
PA (UYZO-) UNIV ZURICH.
Query Match 6.4%; Score 89; DB 4; Length 757;
Best Local Similarity 21.5%; Pred. No. 2;
RESULT 795
ID AAB41293 standard; protein; 758 AA.
DE Human ORFX ORF1057 polypeptide sequence SEQ ID NO:2114.
PN WO200059473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 89; DB 3; Length 758;
Best Local Similarity 21.5%; Pred. No. 2;
RESULT 796
ID AAU74820 standard; protein; 1124 AA.
DE Human REPTR 3 protein.
PN WO200198354-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 89; DB 5; Length 1124;
Best Local Similarity 21.5%; Pred. No. 3.4;
RESULT 797
ID ADA55083 standard; protein; 1203 AA.
DE Human protein, SEQ ID 2651.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%; Score 89; DB 6; Length 1203;
Best Local Similarity 21.5%; Pred. No. 3.7;
RESULT 798
ID ABG31547 standard; protein; 1330 AA.
DE Human patched-like protein.
PN WO200246402-A2.
PD 13-JUN-2002.
PA (FARR) BAYER AG.
Query Match 6.4%; Score 89; DB 5; Length 1330;
Best Local Similarity 21.5%; Pred. No. 4.3;
RESULT 799
ID AEB40780 standard; protein; 361 AA.

DE L. pneumophila protein SEQ ID NO 5112.
PN W02005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 6.4%; Score 88.5; DB 9; Length 361;
Best Local Similarity 20.9%; Pred. No. 0.81;
RESULT 800
ID ADY10982 standard; protein; 372 AA.
DE Plant full length insert polypeptide seqid 66797.
PN US2004034898-A1.
PD 19-FEB-2004.
PA (LIUU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 6.4%; Score 88.5; DB 8; Length 372;
Best Local Similarity 19.3%; Pred. No. 0.84;
RESULT 801
ID AEB37466 standard; protein; 374 AA.
DE L. pneumophila protein SEQ ID NO 1798.
PN W02005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 6.4%; Score 88.5; DB 9; Length 374;
Best Local Similarity 20.9%; Pred. No. 0.85;
RESULT 802
ID AAB96747 standard; protein; 430 AA.
DE Putative P. abyssi permease #26.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match
Best Local Similarity 6.4%; Score 88.5; DB 4; Length 430;
Best Local Similarity 23.8%; Pred. No. 1;
RESULT 803
ID AAR37309 standard; protein; 1165 AA.
DE Cardiac adenylyl cyclase.
PN EP543137-A1.
PD 26-MAY-1993.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match
Best Local Similarity 6.3%; Score 88; DB 2; Length 1165;
Best Local Similarity 20.5%; Pred. No. 4.6;
RESULT 804
ID ABU19097 standard; protein; 233 AA.
DE Protein encoded by Prokaryotic essential gene #4624.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.3%; Score 87.5; DB 6; Length 233;
Best Local Similarity 22.8%; Pred. No. 0.57;
RESULT 805
ID ADD67113 standard; protein; 322 AA.
DE Homogentisate prenyl transferase.
PN W02003080647-A2.
PD 02-OCT-2003.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match
Best Local Similarity 6.3%; Score 87.5; DB 7; Length 322;
Best Local Similarity 22.6%; Pred. No. 0.9;
RESULT 806
ID ADC77581 standard; protein; 453 AA.
DE Mouse TMS2 amino acid sequence.
PN W02003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match
Best Local Similarity 6.3%; Score 87.5; DB 7; Length 453;
Best Local Similarity 22.5%; Pred. No. 1.7;
RESULT 807
ID ADS28619 standard; protein; 482 AA.
DE Bacterial polypeptide #17652.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.3%; Score 87.5; DB 8; Length 482;
Best Local Similarity 21.2%; Pred. No. 1.6;
RESULT 808
ID AEB38041 standard; protein; 521 AA.
DE L. pneumophila protein SEQ ID NO 2373.
PN W02005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 6.3%; Score 87.5; DB 9; Length 521;
Best Local Similarity 22.5%; Pred. No. 1.7;
RESULT 809
ID AEB41335 standard; protein; 521 AA.
DE L. pneumophila protein SEQ ID NO 5667.
PN W02005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 6.3%; Score 87.5; DB 9; Length 521;
Best Local Similarity 22.5%; Pred. No. 1.7;
RESULT 810
ID AEB41995 standard; protein; 535 AA.
DE L. pneumophila protein SEQ ID NO 6327.
PN W02005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 6.2%; Score 87; DB 9; Length 535;
Best Local Similarity 26.0%; Pred. No. 2.1;
RESULT 811
ID ABU33543 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #19070.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.2%; Score 86.5; DB 6; Length 239;
Best Local Similarity 20.4%; Pred. No. 0.77;
RESULT 812
ID ADU05661 standard; protein; 261 AA.
DE Haemophilus influenzae (NTH1) protein - SEQ ID 697.
PN W02004078949-A2.
PD 16-SEP-2004.
PA (CHIL-) CHILDRENS HOSPITAL INC.
Query Match
Best Local Similarity 6.2%; Score 86.5; DB 8; Length 261;
Best Local Similarity 24.2%; Pred. No. 0.87;
RESULT 813
ID ADH87029 standard; protein; 356 AA.
DE Enterococcus faecalis polypeptide #1509.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 6.2%; Score 86.5; DB 7; Length 356;
Best Local Similarity 19.2%; Pred. No. 1.3;
RESULT 814
ID ADS44642 standard; protein; 400 AA.

DE Bacterial polypeptide #23072.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.2%; Score 86.5; DB 8; Length 400;
Best Local Similarity 21.9%; Pred. No. 1.6;
RESULT 815
ID ABB47717 standard; protein; 583 AA.
DE Listeria monocytogenes protein #421.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 6.2%; Score 86.5; DB 5; Length 583;
Best Local Similarity 19.4%; Pred. No. 2.6;
RESULT 816
ID AAG39112 standard; protein; 1346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48347.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.2%; Score 86.5; DB 3; Length 1346;
Best Local Similarity 18.2%; Pred. No. 8.3;
RESULT 817
ID AAG39111 standard; protein; 1390 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48346.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.2%; Score 86.5; DB 3; Length 1390;
Best Local Similarity 18.2%; Pred. No. 8.7;
RESULT 818
ID AAG39110 standard; protein; 1403 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48345.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.2%; Score 86.5; DB 3; Length 1403;
Best Local Similarity 18.2%; Pred. No. 8.8;
RESULT 819
ID ABM73219 standard; protein; 372 AA.
DE Staphylococcus aureus protein #2459.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 6.2%; Score 86; DB 6; Length 372;
Best Local Similarity 18.1%; Pred. No. 1.6;
RESULT 820
ID AAG98347 standard; protein; 396 AA.
DE Escherichia coli protein sequence SEQ ID NO:395.
PN WO200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.2%; Score 86; DB 4; Length 396;
Best Local Similarity 21.9%; Pred. No. 1.8;
RESULT 821
ID ABU14798 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #325.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.2%; Score 86; DB 6; Length 396;
Best Local Similarity 21.9%; Pred. No. 1.8;
RESULT 822
ID ABB90798 standard; protein; 725 AA.
DE Herbicidally active polypeptide SEQ ID NO 9.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.2%; Score 86; DB 5; Length 725;
Best Local Similarity 18.9%; Pred. No. 4.1;
RESULT 823
ID AAB11039 standard; protein; 841 AA.

DE S. xyloosus mprF protein.
PN DE19914817-A1.
PD 05-OCT-2000.
PA (PETR-) PETRY GENMEDICS GMBH.
Query Match
Best Local Similarity 6.2%; Score 86; DB 3; Length 841;
Best Local Similarity 18.3%; Pred. No. 5;
RESULT 824
ID ABP77912 standard; protein; 295 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 2354.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 6.1%; Score 85.5; DB 6; Length 295;
Best Local Similarity 21.6%; Pred. No. 1.3;
RESULT 825
ID ABU37235 standard; protein; 295 AA.
DE Protein encoded by Prokaryotic essential gene #22762.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.1%; Score 85.5; DB 6; Length 295;
Best Local Similarity 21.6%; Pred. No. 1.3;
RESULT 826
ID ABJ39122 standard; protein; 311 AA.
DE Molecule for disease detection and treatment (MDDT)-32 protein sequence.
PN WO2003052049-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 6.1%; Score 85.5; DB 6; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.4;
RESULT 827
ID ADC37363 standard; protein; 311 AA.
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 196.
PN WO2003048202-A2.
PD 12-JUN-2003.
PA (ASAH-) ASAH KASEI KK.
Query Match
Best Local Similarity 6.1%; Score 85.5; DB 7; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.4;
RESULT 828
ID ADR58959 standard; protein; 311 AA.
DE Human Elkl phosphorylation/Elkl kinase activation protein - SEQ ID 62.
PN WO2004072277-A2.
PD 26-AUG-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 6.1%; Score 85.5; DB 8; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.4;
RESULT 829
ID ADU76431 standard; protein; 311 AA.
DE Progesterin-YOLO002c-CGI-45 receptor, INTP047.
PN WO2004101618-A2.
PD 25-NOV-2004.
PA (INPH-) INPHARMATICA LTD.
Query Match
Best Local Similarity 6.1%; Score 85.5; DB 8; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.4;
RESULT 830
ID AAM93524 standard; protein; 329 AA.
DE Human polypeptide, SEQ ID NO: 3257.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 6.1%; Score 85.5; DB 4; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.6;
RESULT 831
ID AAB92687 standard; protein; 329 AA.
DE Human protein sequence SEQ ID NO:11071.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 6.1%; Score 85.5; DB 4; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.6;
RESULT 832
ID ADL31224 standard; protein; 329 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3257.

PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.1%; Score 85.5; DB 8; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.6;
RESULT 833
ID ADA98171 standard; protein; 359 AA.
DE Human secreted protein sequence #12.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 6; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 834
ID ADA44024 standard; protein; 359 AA.
DE Human secreted protein SEQ ID 212.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 6; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 835
ID ADC20341 standard; protein; 359 AA.
DE Human secreted protein - amino acid sequence #17.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 7; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 836
ID ADF10683 standard; protein; 359 AA.
DE Human secreted protein #5.
PN WO200299085-A2.1
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 7; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 837
ID AAB75546 standard; protein; 360 AA.
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:100.
PN WO200077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 6.1%; Score 85.5; DB 4; Length 360;
Best Local Similarity 23.0%; Pred. No. 1.8;
RESULT 838
ID AAW61371 standard; protein; 439 AA.
DE Non-adrenergic SM binding protein.
PN EP848059-A1.
PD 17-JUN-1998.
PA (VETI-) VETIGEN.
Query Match 6.1%; Score 85.5; DB 2; Length 439;
Best Local Similarity 23.0%; Pred. No. 2.3;
RESULT 839
ID AAB75598 standard; protein; 530 AA.
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:152.
PN WO200077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 6.1%; Score 85.5; DB 4; Length 530;
Best Local Similarity 23.0%; Pred. No. 3;
RESULT 840
ID AAY94910 standard; protein; 545 AA.
DE Human secreted protein clone pK366_7 protein sequence SEQ ID NO:26.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GENY) GENETICS INST INC.
Query Match 6.1%; Score 85.5; DB 3; Length 545;
Best Local Similarity 23.0%; Pred. No. 3.1;
RESULT 841
ID AAB54667 standard; protein; 545 AA.

DE Human protein sequence SEQ ID NO:15600.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.1%; Score 85.5; DB 4; Length 545;
Best Local Similarity 23.0%; Pred. No. 3.1;
RESULT 842
ID AAY82460 standard; protein; 579 AA.
DE Human SM-11044-binding receptor protein SEQ ID NO:4.
PN WO200014266-A1.
PD 16-MAR-2000.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 6.1%; Score 85.5; DB 3; Length 579;
Best Local Similarity 23.0%; Pred. No. 3.4;
RESULT 843
ID AAY82459 standard; protein; 582 AA.
DE Human SM-11044-binding receptor protein SEQ ID NO:2.
PN WO200014266-A1.
PD 16-MAR-2000.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 6.1%; Score 85.5; DB 3; Length 582;
Best Local Similarity 23.0%; Pred. No. 3.4;
RESULT 844
ID ABB69104 standard; protein; 700 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34104.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.1%; Score 85.5; DB 4; Length 700;
Best Local Similarity 19.7%; Pred. No. 4.4;
RESULT 845
ID ABE15131 standard; protein; 265 AA.
DE C glutamicum metabolic pathway regulatory (MR) protein SeqID46.
PN US2005153402-A1.
PD 14-JUL-2005.
PA (BADI) BASF AG.
Query Match 6.1%; Score 85; DB 9; Length 265;
Best Local Similarity 24.1%; Pred. No. 1.3;
RESULT 846
ID ABU34786 standard; protein; 338 AA.
DE Protein encoded by Prokaryotic essential gene #20313.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 85; DB 6; Length 338;
Best Local Similarity 23.1%; Pred. No. 1.8;
RESULT 847
ID ABU36544 standard; protein; 338 AA.
DE Protein encoded by Prokaryotic essential gene #22071.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 85; DB 6; Length 338;
Best Local Similarity 23.1%; Pred. No. 1.8;
RESULT 848
ID AAG90802 standard; protein; 419 AA.
DE C glutamicum protein fragment SEQ ID NO: 4556.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.1%; Score 85; DB 4; Length 419;
Best Local Similarity 24.1%; Pred. No. 2.5;
RESULT 849
ID AAE20418 standard; protein; 419 AA.
DE Corynebacterium glutamicum CHRS protein.
PN WO200220572-A2.
PD 14-MAR-2002.
PA (DEGS) DEGUSSA AG.
Query Match 6.1%; Score 85; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 2.5;
RESULT 850
ID AEB15129 standard; protein; 419 AA.
DE C glutamicum metabolic pathway regulatory (MR) protein SeqID44.

PN US2005153402-A1.
PD 14-JUL-2005.
PA (BADI) BASF AG.
Query Match 6.1%; Score 85; DB 9; Length 419;
Best Local Similarity 24.1%; Pred. No. 2.5;
RESULT 851
ID ABB55143 standard; protein; 443 AA.
DE Lactococcus lactis protein ysfC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 85; DB 5; Length 443;
Best Local Similarity 24.4%; Pred. No. 2.7;
RESULT 852
ID AAU78998 standard; protein; 498 AA.
DE Mouse Rh type C gene (RHGC) protein.
PN WO20020719-A2.
PD 14-MAR-2002.
PA (NYBL-) NEW YORK BLOOD CENT INC.
Query Match 6.1%; Score 85; DB 5; Length 498;
Best Local Similarity 20.2%; Pred. No. 3.1;
RESULT 853
ID ADE56874 standard; protein; 1166 AA.
DE Rat Protein Q03343, SEQ ID NO 2729.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GERO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 85; DB 7; Length 1166;
Best Local Similarity 19.8%; Pred. No. 10;
RESULT 854
ID AAB02010 standard; protein; 1180 AA.
DE Type VI adenylyl cyclase.
PN US6107076-A.
PD 22-AUG-2000.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 6.1%; Score 85; DB 3; Length 1180;
Best Local Similarity 19.8%; Pred. No. 10;
RESULT 855
ID ADH88320 standard; protein; 296 AA.
DE Enterococcus faecalis polypeptide #2800.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.1%; Score 84.5; DB 7; Length 296;
Best Local Similarity 25.2%; Pred. No. 1.8;
RESULT 856
ID ABM68417 standard; protein; 324 AA.
DE Photorhabdus luminescens protein sequence #1514.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.1%; Score 84.5; DB 6; Length 324;
Best Local Similarity 23.8%; Pred. No. 2;
RESULT 857
ID AAY07771 standard; protein; 356 AA.
DE Human secreted protein fragment encoded from gene 28.
PN WO9909155-A1.
PD 25-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 84.5; DB 2; Length 356;
Best Local Similarity 19.8%; Pred. No. 2.3;
RESULT 858
ID ABG75197 standard; protein; 408 AA.
DE Wheat homogenisate geranylgeranyl transferase.
PN WO2003082899-A2.
PD 09-OCT-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 6.1%; Score 84.5; DB 7; Length 408;
Best Local Similarity 25.3%; Pred. No. 2.7;
RESULT 859
PN US2005153402-A1.
PD 14-JUL-2005.
PA (BADI) BASF AG.
Query Match 6.1%; Score 85; DB 9; Length 419;
Best Local Similarity 24.1%; Pred. No. 2.5;
RESULT 851
ID ABB55143 standard; protein; 443 AA.
DE Lactococcus lactis protein ysfC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 85; DB 5; Length 443;
Best Local Similarity 24.4%; Pred. No. 2.7;
RESULT 852
ID AAU78998 standard; protein; 498 AA.
DE Mouse Rh type C gene (RHGC) protein.
PN WO20020719-A2.
PD 14-MAR-2002.
PA (NYBL-) NEW YORK BLOOD CENT INC.
Query Match 6.1%; Score 85; DB 5; Length 498;
Best Local Similarity 20.2%; Pred. No. 3.1;
RESULT 853
ID ADE56874 standard; protein; 1166 AA.
DE Rat Protein Q03343, SEQ ID NO 2729.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GERO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 85; DB 7; Length 1166;
Best Local Similarity 19.8%; Pred. No. 10;
RESULT 854
ID AAB02010 standard; protein; 1180 AA.
DE Type VI adenylyl cyclase.
PN US6107076-A.
PD 22-AUG-2000.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 6.1%; Score 85; DB 3; Length 1180;
Best Local Similarity 19.8%; Pred. No. 10;
RESULT 855
ID ADH88320 standard; protein; 296 AA.
DE Enterococcus faecalis polypeptide #2800.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.1%; Score 84.5; DB 7; Length 296;
Best Local Similarity 25.2%; Pred. No. 1.8;
RESULT 856
ID ABM68417 standard; protein; 324 AA.
DE Photorhabdus luminescens protein sequence #1514.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.1%; Score 84.5; DB 6; Length 324;
Best Local Similarity 23.8%; Pred. No. 2;
RESULT 857
ID AAY07771 standard; protein; 356 AA.
DE Human secreted protein fragment encoded from gene 28.
PN WO9909155-A1.
PD 25-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 84.5; DB 2; Length 356;
Best Local Similarity 19.8%; Pred. No. 2.3;
RESULT 858
ID ABG75197 standard; protein; 408 AA.
DE Wheat homogenisate geranylgeranyl transferase.
PN WO2003082899-A2.
PD 09-OCT-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 6.1%; Score 84.5; DB 7; Length 408;
Best Local Similarity 25.3%; Pred. No. 2.7;
RESULT 859
ID AAG46717 standard; protein; 446 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58803.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 84.5; DB 3; Length 446;
Best Local Similarity 19.0%; Pred. No. 3.1;
RESULT 860
ID AAY95015 standard; protein; 453 AA.
DE Human secreted protein vc61_1, SEQ ID NO:70.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 6.1%; Score 84.5; DB 3; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 861
ID AAG65236 standard; protein; 453 AA.
DE Protein tyrosine kinase 50.
PN CN1298944-A.
PD 13-JUN-2001.
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 862
ID AAU29085 standard; protein; 453 AA.
DE Human PRO polypeptide sequence #42.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 863
ID AAM39489 standard; protein; 453 AA.
DE Human polypeptide SEQ ID NO 2634.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 864
ID AAB65170 standard; protein; 453 AA.
DE Human PRO732 (UNQ396) protein sequence SEQ ID NO:73.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 865
ID ABB90299 standard; protein; 453 AA.
DE Human polypeptide SEQ ID NO 2675.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 84.5; DB 5; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 866
ID ABU58441 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 867
ID ABU87989 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 868
ID ABU84304 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032112-A1.
PD 13-FEB-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 869
ID ABR66178 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 870
ID ABR65568 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 871
ID ABU99508 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 872
ID ABU57985 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027183-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 873
ID ABUS9063 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO732.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 874
ID ABUS2575 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 875
ID ABUS2747 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 876
ID ABUS9868 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 877
ID ABR68117 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 878
ID ABUS0494 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 879
ID ABUS96170 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 880
ID ABUS2601 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 881
ID ABO08678 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 882
ID ABO02730 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 883
ID ABR74884 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 884
ID ABR94646 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 885
ID ABUS13876 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 886
ID ABUS5619 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 887
ID ABUS98779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 888
ID ABUS7994 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;

RESULT 889
ID ABU91700 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 890
ID ABU89393 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 891
ID ABU86234 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 892
ID ABU67447 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 893
ID ABU80475 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 894
ID ABU72461 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 895
ID ABR9393 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 896
ID ABR98783 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 897
ID ABO16306 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 898
ID ABR92206 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;

Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 899
ID ABO18847 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 900
ID ABR78268 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 901
ID ABU95004 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 902
ID ABO00143 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 903
ID ABO11475 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 904
ID ABO02120 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 905
ID ABU88694 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 906
ID ABU83389 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 907
ID ABO06190 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 908
ID ABR59226 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 909

ID	ABO09288 standard; protein; 453 AA.
DE	Human secreted/transmembrane protein (PRO) #42.
PB	US2003027324-A1.
PD	06-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 910	
ID	ABO19152 standard; protein; 453 AA.
DE	Novel human secreted and transmembrane protein PRO732.
PN	US2003036118-A1.
PD	20-FEB-2003.
PA	(GETH) GENENTECH INC.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 911	
ID	ABO11170 standard; protein; 453 AA.
DE	Human secreted/transmembrane protein (PRO) #42.
PN	US2003036123-A1.
PD	20-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 912	
ID	ABR66788 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003036148-A1.
PD	20-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 913	
ID	ABO16001 standard; protein; 453 AA.
DE	Human secreted/transmembrane protein (PRO) #42.
PN	US2003040060-A1.
PD	27-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 914	
ID	ABO13707 standard; protein; 453 AA.
DE	Human secreted/transmembrane protein (PRO) #42.
PN	US2003044916-A1.
PD	06-MAR-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 915	
ID	ABU65610 standard; protein; 453 AA.
DE	Human secreted/transmembrane protein, SEQ ID 84.
PN	US2003036156-A1.
PD	20-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 916	
ID	ABO07458 standard; protein; 453 AA.
DE	Human PRO polypeptide #42.
PN	US2003032117-A1.
PD	13-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 917	
ID	ABO03645 standard; protein; 453 AA.
DE	Human secreted/transmembrane protein (PRO) #42.
PN	US2003036128-A1.
PD	20-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 918	
ID	ABR67093 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003027266-A1.
PD	06-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 919	
ID	ABO15696 standard; protein; 453 AA.
DE	Human secreted/transmembrane protein (PRO) #42.
PN	US2003036128-A1.
PD	20-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 920	
ID	ABU55977 standard; protein; 453 AA.
DE	Human secreted/transmembrane protein, PRO732.
PN	US2003022298-A1.
PD	30-JAN-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 921	
ID	ABU65305 standard; protein; 453 AA.
DE	Human PRO polypeptide #42.
PN	US2003032102-A1.
PD	13-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 922	
ID	ABU95250 standard; protein; 453 AA.
DE	Novel Human secreted and transmembrane protein PRO732.
PN	US2003036117-A1.
PD	20-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 923	
ID	ABU71153 standard; protein; 453 AA.
DE	Human PRO732 protein.
PN	US2003036143-A1.
PD	20-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 924	
ID	ABO07763 standard; protein; 453 AA.
DE	Human PRO polypeptide #42.
PN	US2003032130-A1.
PD	13-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 925	
ID	ABR70004 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003032138-A1.
PD	13-FEB-2003.
PA	(GETH) GENENTECH INC.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 926	
ID	ABR69337 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003036132-A1.
PD	20-FEB-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 927	
ID	ASO01478 standard; protein; 453 AA.
DE	Human PRO polypeptide #42.
PN	US2003008353-A1.
PD	09-JAN-2003.
PA	(GETH) GENENTECH INC.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 928	
ID	ABU81280 standard; protein; 453 AA.
DE	Human PRO polypeptide #42.
PN	US2003017542-A1.
PD	23-JAN-2003.
Query Match	6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 929	

PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 930
ID ABR67812 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 931
ID ABR65200 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 932
ID ABR68422 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 933
ID ABR71834 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 934
ID ABR68727 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 935
ID ABR65314 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 936
ID ABR99004 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 937
ID ABR83084 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 938
ID ABR94940 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 939
ID ABR90488 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032108-A1.
PD 13-FEB-2003.

Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 940
ID ABR93999 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 941
ID ABR93650 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 942
ID ABO25907 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 943
ID ABR64895 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027283-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 944
ID ABR68727 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 945
ID ABO06543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 946
ID ABR99088 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 947
ID ABR56972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 948
ID ABR95924 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 949
ID ABR92211 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;

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Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 950
ID ABU87222 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 951
ID ABU83694 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 952
ID ABO08068 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 953
ID ABU81779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 954
ID ABU65943 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 955
ID ABR9772 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 956
ID ABU93960 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 957
ID ABU99813 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 958
ID ABR66483 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 959
ID ABR90901 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 960
ID ABR65873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
ID ABU58916 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 961
ID ABU94328 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 962
ID ABU79210 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 963
ID ABU86539 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 964
ID ABU86844 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 965
ID ABU94633 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 966
ID ABO04560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 967
ID ABR70309 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 968
ID ABU92294 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 969
ID ABU98474 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 970
ID ABR65873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
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PN US2003036165-A1.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 971
ID ABR64590 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 972
ID ABUS9359 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO1120.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 973
ID ABU79515 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 974
ID ABU92906 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 975
ID ABUS865 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 976
ID ABU91085 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 977
ID ABU90178 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 978
ID ABO09593 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 979
ID ABO10865 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 980
ID ABR70919 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 981
ID ABU87527 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 982
ID ABU91395 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 983
ID ABU84609 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 984
ID ABR69699 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 985
ID ABU80076 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 986
ID ABU92125 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 987
ID ABU93345 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 988
ID ABO09898 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 989
ID ABO08983 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 990
ID ABU10831 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
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RESULT 991
ID ABU10551 standard; protein; 453 AA.
DE Human secreted/transmembrane protein #42.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 992
ID ABU1583 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US200217164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 993
ID ABU95560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 994
ID ABU96769 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 995
ID ABR70614 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 996
ID ABO4965 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 997
ID ABO08373 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 998
ID ABU88522 standard; protein; 453 AA.
DE Human secreted and transmembrane polypeptide PRO732.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 999
ID ABO34036 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1000
ID ABO05580 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1001
ID ABR73969 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1002
ID ABR95561 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1003
ID ABR80858 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1004
ID ABR81163 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1005
ID ABM00859 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1006
ID ABR88461 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1007
ID ABM77282 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1008
ID ABO28766 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1009
ID ABO31511 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
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Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1029
ID ABM29037 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1030
ID ABO48074 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1031
ID ABR92816 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1032
ID ABO24577 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1033
ID ADA37584 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1034
ID ABM11588 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1035
ID ABM02689 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1036
ID ABM15985 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1037
ID ABO27546 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1038
ID ABM29037 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1039
ID ABM07013 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1040
ID ABM21107 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1041
ID ABM09453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1042
ID ABO41323 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1043
ID ABO36138 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1044
ID ABO43667 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1045
ID ABM76367 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1046
ID ABM76063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1047
ID ABM25682 standard; protein; 453 AA.
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DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1048
ID ABM25987 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1049
ID ADA21270 standard; protein; 453 AA.
DE Human secreted/transmembrane polypeptide PRO732.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1050
ID ABO03340 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1051
ID ABO02425 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1052
ID ABR90596 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1053
ID ABR73664 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1054
ID ABO16916 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1055
ID ABR94341 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1056
ID ABR75848 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1057
ID ABR71224 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1058
ID ABR93121 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1059
ID ABR93426 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1060
ID ADA10057 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, PRO732.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1061
ID ABR7851 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1062
ID ABO27851 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1063
ID ABO29986 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1064
ID ABO33195 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1065
ID ABM04883 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1066
ID ABM08843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068772-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1067
ID ABO36443 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1068
ID ABO35528 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1069
ID ABO39493 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1070
ID ABM10368 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1071
ID ABM11893 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1072
ID ABO52039 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1073
ID ABO52344 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1074
ID ABO23662 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1075
ID ADA17601 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003054987-A1.
PD 20-NAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1076
ID ABR97148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1077
ID ABR86936 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1078
ID ABM10978 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1079
ID ABM28122 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1080
ID ABO32121 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1081
ID ABM15248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1082
ID ABM06403 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1083
ID ABM04214 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1084
ID ABM22327 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1085

ID ABM07623 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1086
ID ABO40713 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1087
ID ABM35360 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1088
ID ABM33123 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1089
ID ABO52649 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1090
ID ABO50209 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1091
ID ABU9203 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1092
ID ABO4255 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1093
ID ABO05885 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1094
ID ABM18425 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1095
ID ADA27709 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1096
ID ABR97453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1097
ID ABR80553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1098
ID ABM01164 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1099
ID ABR88766 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1100
ID ABM13418 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1101
ID ABM20802 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1102
ID ABO41933 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1103
ID ABO42543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1104

ID	ABM10063 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003067478-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	6.1%; Score 84.5; DB 6;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 1105	Length 453;
ID	A8038578 standard; protein; 453 AA.
DE	Human secreted/transmembrane protein (PRO) #42.
PN	US2003068773-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	6.1%; Score 84.5; DB 6;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 1106	Length 453;
ID	ABM32818 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003073185-A1.
PD	17-APR-2003.
PA	(GETH) GENENTECH INC.
Query Match	6.1%; Score 84.5; DB 6;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 1107	Length 453;
ID	ABM22632 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003087373-A1.
PD	08-MAY-2003.
PA	
Query Match	6.1%; Score 84.5; DB 6;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 1108	Length 453;
ID	ABM74843 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003096353-A1.
PD	22-MAY-2003.
PA	
Query Match	6.1%; Score 84.5; DB 6;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 1109	Length 453;
ID	ADA79628 standard; protein; 453 AA.
DE	Human secreted/transmembrane protein (PRO) #42.
PN	US2003073173-A1.
PD	17-APR-2003.
PA	
Query Match	6.1%; Score 84.5; DB 6;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 1110	Length 453;
ID	ASB96233 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003054458-A1.
PD	20-MAR-2003.
PA	
Query Match	6.1%; Score 84.5; DB 6;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 1111	Length 453;
ID	AW02384 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003059886-A1
PD	27-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	6.1%; Score 84.5; DB 6;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 1112	Length 453;
ID	ASB86326 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003049758-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.
Query Match	6.1%; Score 84.5; DB 6;
Best Local Similarity	19.8%; Pred. No. 3.1;
RESULT 1113	Length 453;
ID	ASB86631 standard; protein; 453 AA.
DE	Human secreted polypeptide PRO732, SEQ ID NO:84.
PN	US2003049772-A1.
PD	13-MAR-2003.
PA	(GETH) GENENTECH INC.

Query Match	6.1%;	Score 84.5;	DB 6;	Length 453;
Best Local Similarity	19.8%;	Pred. No. 3.1;		
RESULT 1114				
ID ABM16595 standard; protein; 453 AA.				
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
FN US2003064448-A1.				
PD 03-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	6.1%;	Score 84.5;	DB 6;	Length 453;
Best Local Similarity	19.8%;	Pred. No. 3.1;		
RESULT 1115				
ID ABM29647 standard; protein; 453 AA.				
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
FN US2003064456-A1.				
PD 03-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	6.1%;	Score 84.5;	DB 6;	Length 453;
Best Local Similarity	19.8%;	Pred. No. 3.1;		
RESULT 1116				
ID ABO29071 standard; protein; 453 AA.				
DE Human secreted/transmembrane protein (PRO) #42.				
FN US2003068693-A1.				
PD 10-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	6.1%;	Score 84.5;	DB 6;	Length 453;
Best Local Similarity	19.8%;	Pred. No. 3.1;		
RESULT 1117				
ID ABM23852 standard; protein; 453 AA.				
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
FN US2003068735-A1.				
PD 10-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	6.1%;	Score 84.5;	DB 6;	Length 453;
Best Local Similarity	19.8%;	Pred. No. 3.1;		
RESULT 1118				
ID ABM23242 standard; protein; 453 AA.				
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
FN US2003068753-A1.				
PD 10-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	6.1%;	Score 84.5;	DB 6;	Length 453;
Best Local Similarity	19.8%;	Pred. No. 3.1;		
RESULT 1119				
ID ABM22022 standard; protein; 453 AA.				
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
FN US2003068742-A1.				
PD 10-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	6.1%;	Score 84.5;	DB 6;	Length 453;
Best Local Similarity	19.8%;	Pred. No. 3.1;		
RESULT 1120				
ID ABO37663 standard; protein; 453 AA.				
DE Human secreted/transmembrane protein (PRO) #42.				
FN US2003068756-A1.				
PD 10-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	6.1%;	Score 84.5;	DB 6;	Length 453;
Best Local Similarity	19.8%;	Pred. No. 3.1;		
RESULT 1121				
ID ABM28427 standard; protein; 453 AA.				
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
FN US2003082715-A1.				
PD 01-MAY-2003.				
Query Match	6.1%;	Score 84.5;	DB 6;	Length 453;
Best Local Similarity	19.8%;	Pred. No. 3.1;		
RESULT 1122				
ID ABM28732 standard; protein; 453 AA.				
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
FN US2003082716-A1.				
PD 01-MAY-2003.				
Query Match	6.1%;	Score 84.5;	DB 6;	Length 453;
Best Local Similarity	19.8%;	Pred. No. 3.1;		
RESULT 1123				
ID ABM28732 standard; protein; 453 AA.				
DE Human secreted polypeptide PRO732, SEQ ID NO:84.				
FN US2003082716-A1.				
PD 01-MAY-2003.				
Query Match	6.1%;	Score 84.5;	DB 6;	Length 453;
Best Local Similarity	19.8%;	Pred. No. 3.1;		
RESULT 1123				

ID ABM66376 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068737-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1124
 ID ABM75758 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003104547-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1125
 ID ABM34038 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003096359-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1126
 ID ABM34343 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003100061-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1127
 ID ABO20274 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003032125-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1128
 ID ABO21189 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003054454-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1129
 ID ABO22104 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003054477-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1130
 ID ABR96538 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003054460-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1131
 ID ADA94289 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003059832-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1132
 ID ABR85716 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049753-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1133
 ID ABR99698 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003049763-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1134
 ID ABM00554 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003073172-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1135
 ID ABM00249 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003073172-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1136
 ID ABO29681 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003068700-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1137
 ID ABM23547 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068736-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1138
 ID ABM29342 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003068679-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1139
 ID ABO38273 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein (PRO) #42.
 PN US2003068767-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1140
 ID ABO45573 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003073182-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1141
 ID ABM20497 standard; protein; 453 AA.
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.
 PN US2003104557-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 6; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;

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RESULT 1142
ID ADA81355 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003092121-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1143
ID ABO16611 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1144
ID ABO18237 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1145
ID ABO22664 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027285-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1146
ID ABO22969 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1147
ID ABR92511 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1148
ID ABR81468 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1149
ID ABM77892 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1150
ID ABR99681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1151
ID ABM26597 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1152
ID ABM13723 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1153
ID ABO28461 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1154
ID ABO30291 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1155
ID ABM07318 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1156
ID ABM031909 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1157
ID ABO37053 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1158
ID ABO41628 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1159
ID ABO35223 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1160
ID ABM25072 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
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RESULT 1161
ID ABO47464 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1162
ID ABO47769 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1163
ID ABO48379 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1164
ID ABO51429 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1165
ID ABO51734 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1166
ID ABO50514 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1167
ID ABR79638 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1168
ID ABM16900 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1169
ID ABO17932 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1170
ID ABO20884 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1171
ID ABR96843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1172
ID ADA38514 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1173
ID ABM12198 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1174
ID ABM16290 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1175
ID ABM24157 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1176
ID ABM14638 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1177
ID ABM04519 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1178
ID ABM06708 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1179
ID ABM09148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;

RESULT 1180
ID ABO39188 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1181
ID ABM75453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1182
ID ABM25377 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1183
ID ABM19887 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104534-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1184
ID ABO46793 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1185
ID ABO47098 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1186
ID ADA8153 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1187
ID ABR71529 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1188
ID ABR72139 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1189
ID ABR98478 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036129-A1.

PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1190
ID ABO06848 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1191
ID ABR84801 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1192
ID ABR73359 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1193
ID ABR76453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1194
ID ABR73054 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1195
ID ABM18120 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1196
ID ABO20579 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1197
ID ABO25322 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1198
ID ABO25627 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1199
ID ABR94036 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.

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PN US2003059879-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1209
ID ABM15553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1210
ID ABM08538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1211
ID ABO42238 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1212
ID ABO17968 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1213
ID ABO45878 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1214
ID ABM66681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1215
ID ADB20196 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1216
ID ABM19582 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1217
ID ABO49294 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
PN US200305700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
PN US2003059879-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1200
ID ADA92635 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1201
ID ABR79943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1202
ID ABM11283 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1203
ID ABO32890 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1204
ID ABO30596 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1205
ID ABO30901 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1206
ID ABM27207 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1207
ID ABM29952 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1208
ID ABM05488 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
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RESULT 1218
ID ABO49599 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1219
ID ADA78448 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1220
ID ABR88156 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003088720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1221
ID ABM26902 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1222
ID ABM03299 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1223
ID ABO39798 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003088689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1224
ID ABO49904 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1225
ID ABO50819 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1226
ID ABO5275 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1227
ID ABR74579 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1228
ID ABR77058 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1229
ID ABM17815 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1230
ID ABR95866 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1231
ID ABO21799 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1232
ID ABO19969 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1233
ID ABO24272 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1234
ID ABR86021 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1235
ID ABM10673 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
RESULT 1236
ID ABM76672 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 453;
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RESULT 1237
ID ABR89376 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1238
ID ABM12503 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1239
ID ABM05793 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1240
ID ABO34918 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1241
ID ABM02994 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1242
ID ABM18972 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1243
ID ABM19277 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1244
ID ABO46488 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1245
ID ABO48989 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1246
ID ABR69032 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1247
ID ABR89071 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1248
ID ABR72444 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1249
ID ABR74274 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1250
ID ABO18542 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1251
ID ABR80248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1252
ID ABM01469 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1253
ID ABM02079 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1254
ID ABR87241 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1255
ID ABM12808 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1256
ID ABM30562 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1257
ID ABM24462 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1258
ID ABO29376 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1259
ID ABO31206 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1260
ID ABM14333 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1261
ID ABM09758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1262
ID ABO38883 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1263
ID ABM34648 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1264
ID ABO51124 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1265
ID ABO03950 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1266
ID ABO10420 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1267
ID ABO53122 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1268
ID ABR77663 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1269
ID ABR78873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1270
ID ABO23967 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1271
ID ABR93731 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1272
ID ABM01774 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1273
ID ABM78197 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1274
ID ABR89986 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;

Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1275
ID ADA22196 standard; protein; 453 AA.
DE Human secreted/transmembrane polypeptide PRO732.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1276
ID ABM27512 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1277
ID ABM13113 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1278
ID ABO31816 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1279
ID ABM14028 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068754-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1280
ID ABM08233 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1281
ID ABO40103 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1282
ID ABM74538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1283
ID ABM33733 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1284
ID ABM20192 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1285
ID ABO48684 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1286
ID ABO22492 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1287
ID ABR72749 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1288
ID ABO15391 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1289
ID ABR85106 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1290
ID ABO15086 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1291
ID ABO17221 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1292
ID ABM17510 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1293
ID ADA06362 standard; protein; 453 AA.
DE Human secreted/transmembrane PRO polypeptide #17.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1294
ID ADA39055 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.

PA US2003059782-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1295
ID ABR85411 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1296
ID ABM76977 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1297
ID ABO28156 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1298
ID ABM22937 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1299
ID ABM30257 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1300
ID ABM21717 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1301
ID ABM21412 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1302
ID ABM14943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1303
ID ABO41018 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068694-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1304
ID ABO36748 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1305
ID ABO37358 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1306
ID ABM75148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1307
ID ABM33428 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1308
ID ABO46183 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1309
ID ADA82519 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1310
ID ADB96081 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1311
ID ABM31782 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1312
ID ABM31172 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;

RESULT 1313
ID ADB5827 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US200305472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1314
ID ABM32087 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1315
ID ABM32392 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1316
ID ABM31477 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1317
ID ABM30867 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1318
ID ADC57553 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1319
ID ADC54917 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1320
ID ADC11784 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1321
ID ADC56206 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1322
ID ADC07261 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1323
ID ADC11251 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1324
ID ADC14373 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1325
ID ADD07905 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1326
ID ADC81730 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1327
ID ADD07372 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1328
ID ADC77580 standard; protein; 453 AA.
DE Human TMS2 amino acid sequence.
PN WO2003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1329
ID ADC82283 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1330
ID ADD05557 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1331
ID ADD08443 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1332
ID ADD06692 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193300-A1.
PD 19-DEC-2002.

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1333
ID ADC82939 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1334
ID ADD55046 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1335
ID ADD56004 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1336
ID ADD54442 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1337
ID ADE26596 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1338
ID ADE26063 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1339
ID ADF67000 standard; protein; 453 AA.
DE Human PRO732 amino acid sequence SEQ ID NO:73.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1340
ID ADG02552 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1341
ID ADG01259 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1342
ID ADF95434 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.

PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1343
ID ADG12249 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1344
ID ADH08909 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1345
ID ADI35254 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1346
ID ADH99746 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1347
ID ADL32690 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1348
ID ADM30224 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1349
ID ADE74221 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1350
ID ADE74833 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1351
ID ADF35199 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.1;
RESULT 1352
ID ADG11449 standard; protein; 453 AA.

DE Human PRO732 polypeptide.
 PN US2003228655-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1353
 ID ADF96046 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003215909-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1354
 ID ADG04317 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003215912-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1355
 ID ADG00477 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003215911-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1356
 ID ADG82733 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003215910-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1357
 ID ADH26014 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2003068770-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1358
 ID ADH19319 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003228656-A1.
 PD 11-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1359
 ID ADH32983 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2003068768-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1360
 ID ADH20812 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003224358-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1361
 ID ADH19852 standard; protein; 453 AA.
 DE Human secreted/transmembrane protein PRO732.
 PN US2003219856-A1.
 PD 27-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1362
 ID ADJ54722 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2004023321-A1.
 PD 05-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1363
 ID ADJ64493 standard; protein; 453 AA.
 DE Human PRO polypeptide #42.
 PN US2004038337-A1.
 PD 26-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1364
 ID ADM31389 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2004048334-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1365
 ID ADM36436 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2004053358-A1.
 PD 18-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1366
 ID ADM40241 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2004048335-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1367
 ID ADN37849 standard; protein; 453 AA.
 DE Novel human secreted and transmembrane protein PRO732.
 PN US2004091959-A1.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1368
 ID ADR09184 standard; protein; 453 AA.
 DE Human protein useful for treating neurological disease Seq 2690.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1369
 ID ABM80816 standard; protein; 453 AA.
 DE Tumour-associated antigenic target (TAT) polypeptide PRO81457, SEQ:2102.
 PN WO2004030615-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.1%; Score 84.5; DB 8; Length 453;
 Best Local Similarity 19.8%; Pred. No. 3.1;
 RESULT 1370
 ID ADR99176 standard; protein; 453 AA.
 DE KIAA1253, SEQ ID 182.
 PN WO2004078035-A2.
 PD 16-SEP-2004.
 PA (FARB) BAYER PHARM CORP.

Query Match
Best Local Similarity 6.1%; Score 84.5; DB 8; Length 453;
RESULT 1371
ID ADV69528 standard; protein; 453 AA.
DE Human tyrosine kinase 50 amino acid sequence - SEQ ID 2.
PN CN1510134-A.
PD 07-JUL-2004.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 8; Length 453;
RESULT 1372
ID AEA38376 standard; protein; 453 AA.
DE Human secreted/transmembrane protein cDNA, #86.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 9; Length 453;
RESULT 1373
ID ADG10618 standard; protein; 472 AA.
DE Human STAT6-activating protein, SEQ ID NO:208.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 7; Length 472;
RESULT 1374
ID AAM41275 standard; protein; 477 AA.
DE Human polypeptide SEQ ID NO 6206.
PN WO20015313-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 4; Length 477;
RESULT 1375
ID AAG46716 standard; protein; 521 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58802.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 3; Length 521;
RESULT 1376
ID ABB93783 standard; protein; 562 AA.
DE Herbicidially active polypeptide SEQ ID NO 2994.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 5; Length 562;
RESULT 1377
ID AAG46715 standard; protein; 571 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58801.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 3; Length 571;
RESULT 1378
ID ADX95745 standard; protein; 600 AA.
DE Plant full length insert polypeptide seqid 58409.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ) LIU J.
PA (ZHOU) ZHOU Y.
PA (KOVA) KOVALIC D K.
PA (SCRE) SCREEN S E.
PA (TABA) TABASKA J E.
PA (CAOY) CAO Y.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 8; Length 600;
RESULT 1379
ID ADA36714 standard; protein; 241 AA.
DE Acinetobacter baumannii protein #3875.
PN US6562958-B1.

PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 6.0%; Score 84; DB 6; Length 241;
RESULT 1380
ID ABG61495 standard; protein; 318 AA.
DE Iron uptake ABC transporter polypeptide #2.
PN WO200234773-A2.
PD 02-MAY-2002.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
Query Match
Best Local Similarity 6.0%; Score 84; DB 5; Length 318;
RESULT 1381
ID ABU02362 standard; protein; 318 AA.
DE S. pneumoniae type 4 strain protein from coding region #1940.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 6.0%; Score 84; DB 6; Length 318;
RESULT 1382
ID AD210513 standard; protein; 403 AA.
DE P. gingivalis hypothetical protein SEQ ID 296.
PN WO2005019249-A2.
PD 03-MAR-2005.
PA (UYFL) UNIV FLORIDA.
Query Match
Best Local Similarity 6.0%; Score 84; DB 9; Length 403;
RESULT 1383
ID ABG10541 standard; protein; 480 AA.
DE Novel human diagnostic protein #10532.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.0%; Score 84; DB 4; Length 480;
RESULT 1384
ID ADU04919 standard; protein; 506 AA.
DE M. catarrhalis protein #685.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 6.0%; Score 84; DB 8; Length 506;
RESULT 1385
ID ADS23392 standard; protein; 516 AA.
DE Bacterial polypeptide #12425.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match
Best Local Similarity 6.0%; Score 84; DB 8; Length 516;
RESULT 1386
ID AB067632 standard; protein; 537 AA.
DE Klebsiella pneumoniae polypeptide seqid 14149.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 6.0%; Score 84; DB 7; Length 537;
RESULT 1387
ID ABU38257 standard; protein; 575 AA.
DE Protein encoded by Prokaryotic essential gene #23784.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.0%; Score 84; DB 6; Length 575;
RESULT 1388

RESULT 1388
 ID ABO73781 standard; protein; 602 AA.
 DE Pseudomonas aeruginosa polypeptide #5956.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 6.0%; Score 84; DB 7; Length 602;
 Best Local Similarity 20.3%; Pred. No. 5.3;
 RESULT 1389
 ID ABO70835 standard; protein; 720 AA.
 DE Pseudomonas aeruginosa polypeptide #3010.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 6.0%; Score 84; DB 7; Length 720;
 Best Local Similarity 21.8%; Pred. No. 6.8;
 RESULT 1390
 ID ABU32051 standard; protein; 1137 AA.
 DE Protein encoded by Prokaryotic essential gene #17578.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.0%; Score 84; DB 6; Length 1137;
 Best Local Similarity 18.6%; Pred. No. 13;
 RESULT 1391
 ID ABO67057 standard; protein; 1138 AA.
 DE Klebsiella pneumoniae polypeptide seqid 13574.
 PN US6610836-B1.
 PD 26-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 6.0%; Score 84; DB 7; Length 1138;
 Best Local Similarity 18.6%; Pred. No. 13;
 RESULT 1392
 ID ADT60220 standard; protein; 294 AA.
 DE Plant polypeptide, SEQ ID 10297.
 PN US2004216190-A1.
 PD 28-OCT-2004.
 PA (KOVA/) KOVALIC D K.
 Query Match 6.0%; Score 83.5; DB 8; Length 294;
 Best Local Similarity 25.4%; Pred. No. 2.3;
 RESULT 1393
 ID ABU37874 standard; protein; 295 AA.
 DE Protein encoded by Prokaryotic essential gene #23401.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.0%; Score 83.5; DB 6; Length 295;
 Best Local Similarity 21.6%; Pred. No. 2.3;
 RESULT 1394
 ID ADV88472 standard; protein; 333 AA.
 DE Streptococcus agalactiae protein sequence, SEQ ID 866.
 PN FR2824074-A1.
 PD 31-OCT-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 6.0%; Score 83.5; DB 8; Length 333;
 Best Local Similarity 21.4%; Pred. No. 2.7;
 RESULT 1395
 ID ADV79725 standard; protein; 333 AA.
 DE Streptococcus agalactiae protein, SEQ ID 866.
 PN WO200292818-A2.
 PD 21-NOV-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 6.0%; Score 83.5; DB 8; Length 333;
 Best Local Similarity 21.4%; Pred. No. 2.7;
 RESULT 1396
 ID ADV81883 standard; protein; 333 AA.
 DE Streptococcus agalactiae protein, SEQ ID 3024.
 PN WO200292818-A2.
 PD 21-NOV-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.

Query Match 6.0%; Score 83.5; DB 8; Length 333;
 Best Local Similarity 21.4%; Pred. No. 2.7;
 RESULT 1397
 ID AAR97984 standard; protein; 618 AA.
 DE DmORF1 potassium channel protein.
 PN WO9613520-A1.
 PD 09-MAY-1996.
 PA (AMCY) AMERICAN CYANAMID CO.
 Query Match 6.0%; Score 83.5; DB 2; Length 618;
 Best Local Similarity 19.9%; Pred. No. 6.3;
 RESULT 1398
 ID AAU07616 standard; protein; 618 AA.
 DE Drosophila melanogaster potassium ion channel ORF1 (DmORF1) protein.
 PN WO200161006-A2.
 PD 23-AUG-2001.
 PA (BADI) BASF CORP.
 Query Match 6.0%; Score 83.5; DB 4; Length 618;
 Best Local Similarity 19.9%; Pred. No. 6.3;
 RESULT 1399
 ID ABG30123 standard; protein; 1027 AA.
 DE Novel human diagnostic protein #30114.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.0%; Score 83.5; DB 4; Length 1027;
 Best Local Similarity 19.8%; Pred. No. 13;
 RESULT 1400
 ID ABU28293 standard; protein; 1090 AA.
 DE Protein encoded by Prokaryotic essential gene #13820.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.0%; Score 83.5; DB 6; Length 1090;
 Best Local Similarity 18.5%; Pred. No. 14;
 RESULT 1401
 ID AAG44538 standard; protein; 250 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 55802.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 6.0%; Score 83; DB 3; Length 250;
 Best Local Similarity 21.7%; Pred. No. 2.1;
 RESULT 1402
 ID AAG66371 standard; protein; 305 AA.
 DE Human partial olfactory receptor-like protein OLF3 #2.
 PN WO200155179-A2.
 PD 02-AUG-2001.
 PA (CURA-) CURAGEN CORP.
 Query Match 6.0%; Score 83; DB 4; Length 305;
 Best Local Similarity 20.6%; Pred. No. 2.7;
 RESULT 1403
 ID AAY85935 standard; protein; 318 AA.
 DE S. pneumoniae derived protein #144.
 PN WO9806734-A1.
 PD 19-FEB-1998.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 Query Match 6.0%; Score 83; DB 2; Length 318;
 Best Local Similarity 24.4%; Pred. No. 2.9;
 RESULT 1404
 ID ADK46461 standard; protein; 318 AA.
 DE Streptococcus pneumoniae protein, Seq ID No 2976.
 PN US6699703-B1.
 PD 02-MAR-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 6.0%; Score 83; DB 8; Length 318;
 Best Local Similarity 24.4%; Pred. No. 2.9;
 RESULT 1405
 ID AAG71916 standard; protein; 319 AA.
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1597.
 PN WO200127158-A2.
 PD 19-APR-2001.
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 Query Match 6.0%; Score 83; DB 4; Length 319;

Best Local Similarity 20.6%; Pred. No. 2.9;
RESULT 1406
ID AAB46999 standard; protein; 321 AA.
DE Human OLFXY protein.
PN DE19937839-A1.
PD 15-FEB-2001.
PA (BRUE/) BRUESS M.
PA (BOEN/) BOENISCH H.
Query Match 6.0%; Score 83; DB 4; Length 321;
Best Local Similarity 20.6%; Pred. No. 2.9;
RESULT 1407
ID ABP95927 standard; protein; 321 AA.
DE Human GPCR polypeptide SEQ ID NO 664.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.0%; Score 83; DB 5; Length 321;
Best Local Similarity 20.6%; Pred. No. 2.9;
RESULT 1408
ID ADU24127 standard; protein; 321 AA.
DE Human aspartic peptidase enzyme #19.
PN US2004219609-A1.
PD 04-NOV-2004.
PA (DAYA/) DAY A G.
PA (ESTE/) ESTELL D A.
PA (LYON/) LYONS E H.
PA (YAOJ/) YAO J.
Query Match 6.0%; Score 83; DB 8; Length 321;
Best Local Similarity 20.6%; Pred. No. 2.9;
RESULT 1409
ID ADR96441 standard; protein; 336 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 5076.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 8; Length 336;
Best Local Similarity 24.4%; Pred. No. 3.1;
RESULT 1410
ID AEA60311 standard; protein; 336 AA.
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:5076.
PN US2005136404-A1.
PD 23-JUN-2005.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.0%; Score 83; DB 9; Length 336;
Best Local Similarity 24.4%; Pred. No. 3.1;
RESULT 1411
ID ABU43979 standard; protein; 355 AA.
DE Protein encoded by Prokaryotic essential gene #29506.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 83; DB 6; Length 355;
Best Local Similarity 23.0%; Pred. No. 3.3;
RESULT 1412
ID ABO2213 standard; protein; 417 AA.
DE Klebsiella pneumoniae polypeptide seqid 8730.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 7; Length 417;
Best Local Similarity 20.8%; Pred. No. 4.2;
RESULT 1413
ID AAY66647 standard; protein; 455 AA.
DE Membrane-bound protein PRO732.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH-) GENENTECH INC.
Query Match 6.0%; Score 83; DB 3; Length 455;
Best Local Similarity 19.8%; Pred. No. 4.7;
RESULT 1414
ID AAB96670 standard; protein; 490 AA.
DE Putative P. abyssi succinyl-CoA synthetase #5.

PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 6.0%; Score 83; DB 4; Length 490;
Best Local Similarity 23.6%; Pred. No. 5.2;
RESULT 1415
ID ABO70524 standard; protein; 542 AA.
DE Pseudomonas aeruginosa polypeptide #2699.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 7; Length 542;
Best Local Similarity 20.2%; Pred. No. 6;
RESULT 1416
ID ADA33498 standard; protein; 632 AA.
DE Acinetobacter baumannii protein #659.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 6; Length 632;
Best Local Similarity 25.1%; Pred. No. 7.4;
RESULT 1417
ID ABB65640 standard; protein; 774 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23712.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 83; DB 4; Length 774;
Best Local Similarity 22.4%; Pred. No. 9.7;
RESULT 1418
ID AAU38963 standard; protein; 774 AA.
DE Drosophila G-protein coupled receptor, GCPR #41.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 83; DB 4; Length 774;
Best Local Similarity 22.4%; Pred. No. 9.7;
RESULT 1419
ID ADC35871 standard; protein; 774 AA.
DE Drosophila G protein coupled receptor seq id 43.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 83; DB 7; Length 774;
Best Local Similarity 22.4%; Pred. No. 9.7;
RESULT 1420
ID AAB38199 standard; protein; 802 AA.
DE Fruit fly G protein-coupled receptor (GPCR) protein #48.
PN WO2003052078-A2.
PD 26-JUN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.0%; Score 83; DB 7; Length 802;
Best Local Similarity 22.4%; Pred. No. 10;
RESULT 1421
ID ABP70924 standard; protein; 2159 AA.
DE Maize DEK1 from B73.
PN WO2003011015-A2.
PD 13-FEB-2003.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 6.0%; Score 83; DB 6; Length 2159;
Best Local Similarity 20.6%; Pred. No. 40;
RESULT 1422
ID ADT57399 standard; protein; 2159 AA.
DE Plant polypeptide, SEQ ID 7476.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 6.0%; Score 83; DB 8; Length 2159;
Best Local Similarity 20.6%; Pred. No. 40;
RESULT 1423
ID ADS43623 standard; protein; 391 AA.
DE Bacterial polypeptide #22053.

PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 5.9%; Score 82.5; DB 8; Length 391;
 Best Local Similarity 23.2%; Pred. No. 4.3;
 RESULT 1424
 ID ABU28011 standard; protein; 395 AA.
 DE Protein encoded by Prokaryotic essential gene #13538.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 82.5; DB 6; Length 395;
 Best Local Similarity 19.7%; Pred. No. 4.4;
 RESULT 1425
 ID AAW21009 standard; protein; 461 AA.
 DE H. pylori cell envelope transporter protein, hp5ell1726orf7.
 PN WO9640893-A1.
 PD 19-DEC-1996.
 PA (ASTR-) ASTRA AB.
 Query Match 5.9%; Score 82.5; DB 2; Length 461;
 Best Local Similarity 21.5%; Pred. No. 5.4;
 RESULT 1426
 ID ABO69393 standard; protein; 492 AA.
 DE Pseudomonas aeruginosa polypeptide #1568.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 82.5; DB 7; Length 492;
 Best Local Similarity 19.1%; Pred. No. 5.9;
 RESULT 1427
 ID ADN18812 standard; protein; 596 AA.
 DE Bacterial polypeptide #1465.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 5.9%; Score 82.5; DB 8; Length 596;
 Best Local Similarity 20.6%; Pred. No. 7.7;
 RESULT 1428
 ID ABG06558 standard; protein; 875 AA.
 DE Novel human diagnostic protein #6549.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 82.5; DB 4; Length 875;
 Best Local Similarity 26.0%; Pred. No. 13;
 RESULT 1429
 ID ADJ69204 standard; protein; 1457 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID1010.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 5.9%; Score 82.5; DB 7; Length 1457;
 Best Local Similarity 26.0%; Pred. No. 26;
 RESULT 1430
 ID ADJ69205 standard; protein; 1457 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID1011.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 5.9%; Score 82.5; DB 7; Length 1457;
 Best Local Similarity 26.0%; Pred. No. 26;
 RESULT 1431
 ID ADJ58460 standard; protein; 1457 AA.

DE BAB13458.1(P450G5) protein.
 PN WO2004011648-A2.
 PD 05-FEB-2004.
 PA (INPH-) INPHARMATICA LTD.
 Query Match 5.9%; Score 82.5; DB 8; Length 1457;
 Best Local Similarity 26.0%; Pred. No. 26;
 RESULT 1432
 ID ADC31246 standard; protein; 2548 AA.
 DE Human novel polypeptide sequence, SEQ ID NO:1328.
 PN WO2003029271-A2.
 PD 10-APR-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 82.5; DB 7; Length 2548;
 Best Local Similarity 26.0%; Pred. No. 57;
 RESULT 1433
 ID ABO84919 standard; protein; 219 AA.
 DE Human cancer-associated protein (CAP) HP07-069.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 5.9%; Score 82; DB 8; Length 219;
 Best Local Similarity 22.1%; Pred. No. 2.2;
 RESULT 1434
 ID AAB87783 standard; protein; 299 AA.
 DE Rat T2R03 amino acid sequence SEQ ID NO:81.
 PN WO200118050-A2.
 PD 15-MAR-2001.
 PA (REGC-) UNIV CALIFORNIA.
 PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
 Query Match 5.9%; Score 82; DB 4; Length 299;
 Best Local Similarity 22.8%; Pred. No. 3.4;
 RESULT 1435
 ID ADJ84452 standard; protein; 299 AA.
 DE Rat T2R G-protein coupled receptor seq id 5.
 PN US2004038312-A1.
 PD 26-FEB-2004.
 PA (ZUKER/) ZUKER C S.
 PA (ADLE/) ADLER J E.
 PA (HOON/) HOON M.
 PA (RYBA/) RYBA N.
 PA (MUEL/) MUELLER K.
 Query Match 5.9%; Score 82; DB 8; Length 299;
 Best Local Similarity 22.8%; Pred. No. 3.4;
 RESULT 1436
 ID ADR29142 standard; protein; 299 AA.
 DE Taste receptor modulation-related rat T2R03 protein sequence SeqID81.
 PN WO2004069191-A2.
 PD 19-AUG-2004.
 PA (SENO-) SENOMYX INC.
 Query Match 5.9%; Score 82; DB 8; Length 299;
 Best Local Similarity 22.8%; Pred. No. 3.4;
 RESULT 1437
 ID AAB10684 standard; protein; 356 AA.
 DE A. thaliana PUP1 protein.
 PN DE19907209-A1.
 PD 24-AUG-2000.
 PA (FROM/) FROMMER W.
 Query Match 5.9%; Score 82; DB 3; Length 356;
 Best Local Similarity 19.4%; Pred. No. 4.3;
 RESULT 1438
 ID ABB91157 standard; protein; 356 AA.
 DE Herbicidically active polypeptide SEQ ID NO 368.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB-) BAYER AG.
 Query Match 5.9%; Score 82; DB 5; Length 356;
 Best Local Similarity 19.4%; Pred. No. 4.3;
 RESULT 1439
 ID ABU28157 standard; protein; 417 AA.
 DE Protein encoded by Prokaryotic essential gene #13684.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.

Query Match 5.9%; Score 82; DB 6; Length 417;
Best Local Similarity 27.1%; Pred. No. 5.4;
RESULT 1440
ID ADX68336 standard; protein; 440 AA.
DE Plant full length insert polypeptide seqid 39179.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 5.9%; Score 82; DB 8; Length 440;
Best Local Similarity 24.4%; Pred. No. 5.8;
RESULT 1441
ID ADK16901 standard; protein; 465 AA.
DE Nancarchaeum equitans cancer-associated (CA) protein #426.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 5.9%; Score 82; DB 8; Length 465;
Best Local Similarity 23.7%; Pred. No. 6.3;
RESULT 1442
ID ABO81608 standard; protein; 474 AA.
DE Pseudomonas aeruginosa polypeptide #13783.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 82; DB 7; Length 474;
Best Local Similarity 20.1%; Pred. No. 6.4;
RESULT 1443
ID ADY13455 standard; protein; 478 AA.
DE Plant full length insert polypeptide seqid 69270.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 5.9%; Score 82; DB 8; Length 478;
Best Local Similarity 23.3%; Pred. No. 6.5;
RESULT 1444
ID ADN3219 standard; protein; 573 AA.
DE Bacterial polypeptide #5872.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 82; DB 8; Length 573;
Best Local Similarity 18.5%; Pred. No. 8.4;
RESULT 1445
ID ADN3218 standard; protein; 573 AA.
DE Bacterial polypeptide #5871.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 82; DB 8; Length 573;
Best Local Similarity 18.5%; Pred. No. 8.4;
RESULT 1446
ID ABUS0193 standard; protein; 1139 AA.
DE Protein encoded by Prokaryotic essential gene #35720.
PN WO200277183-A2.
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 82; DB 6; Length 1139;
Best Local Similarity 19.5%; Pred. No. 22;
RESULT 1447
ID AAE04312 standard; protein; 1167 AA.
DE Human modified cardiac adenylyclase VI (ACVI) isoform.
PN WO200148164-A2.
PD 05-JUL-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.9%; Score 82; DB 4; Length 1167;
Best Local Similarity 20.2%; Pred. No. 22;
RESULT 1448
ID ABG32870 standard; protein; 1167 AA.
DE Chimeric Adenylyclase isoform 6, AC-VI.
PN US2002103147-A1.
PD 01-AUG-2002.
PA (HAMW/) HAMMOND H K.
PA (INSE/) INSEL P A.
PA (PING/) PING P.
PA (POST/) POST S R.
PA (GAOM/) GAO M.
Query Match 5.9%; Score 82; DB 5; Length 1167;
Best Local Similarity 20.2%; Pred. No. 22;
RESULT 1449
ID AAW30599 standard; protein; 1168 AA.
DE Human type VI adenylyl cyclase.
PN WO9901547-A1.
PD 14-JAN-1999.
PA (CORT-) COR THERAPEUTICS INC.
Query Match 5.9%; Score 82; DB 2; Length 1168;
Best Local Similarity 20.2%; Pred. No. 22;
RESULT 1450
ID AAE04311 standard; protein; 1168 AA.
DE Human cardiac adenylyclase VI (ACVI) isoform #2.
PN WO200148164-A2.
PD 05-JUL-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.9%; Score 82; DB 4; Length 1168;
Best Local Similarity 20.2%; Pred. No. 22;
RESULT 1451
ID ABG32869 standard; protein; 1168 AA.
DE Human Adenylyclase isoform 6, AC-VI, #2.
PN US2002103147-A1.
PD 01-AUG-2002.
PA (HAMW/) HAMMOND H K.
PA (INSE/) INSEL P A.
PA (PING/) PING P.
PA (POST/) POST S R.
PA (GAOM/) GAO M.
Query Match 5.9%; Score 82; DB 5; Length 1168;
Best Local Similarity 20.2%; Pred. No. 22;
RESULT 1452
ID ADE56876 standard; protein; 1168 AA.
DE Human Protein O43306, SEQ ID NO 2731.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 82; DB 7; Length 1168;
Best Local Similarity 20.2%; Pred. No. 22;
RESULT 1453
ID ADQ98950 standard; protein; 1168 AA.
DE Antagonist of cell cycle progression polypeptide #140.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 5.9%; Score 82; DB 8; Length 1168;
Best Local Similarity 20.2%; Pred. No. 22;
RESULT 1454
ID ADX98516 standard; protein; 1168 AA.
DE Human adenylylase cyclase 6 (ADCY6) protein.
PN WO2005017121-A2.
PD 24-FEB-2005.

PA (EXEL-) EXELIXIS INC.
 Query Match 5.9%; Score 82; DB 9; Length 1168;
 Best Local Similarity 20.2%; Pred. No. 22;
 RESULT 1455
 ID ADK46612 standard; protein; 199 AA.
 DE Streptococcus pneumoniae protein, Seq ID No 3127.
 PN US699703-B1.
 PD 02-MAR-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 81.5; DB 8; Length 199;
 Best Local Similarity 20.2%; Pred. No. 2.2;
 RESULT 1456
 ID ABU02196 standard; protein; 205 AA.
 DE S. pneumoniae type 4 strain protein from coding region #1774.
 PN WO200277021-A2.
 PD 03-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Query Match 5.9%; Score 81.5; DB 6; Length 205;
 Best Local Similarity 20.2%; Pred. No. 2.3;
 RESULT 1457
 ID AAY81546 standard; protein; 206 AA.
 DE Streptococcus pneumoniae type 4 protein sequence #46.
 PN WO20006737-A2.
 PD 10-FEB-2000.
 PA (MICR-) MICROBIAL TECHNIQS LTD.
 Query Match 5.9%; Score 81.5; DB 3; Length 206;
 Best Local Similarity 20.2%; Pred. No. 2.3;
 RESULT 1458
 ID ADR96056 standard; protein; 208 AA.
 DE Novel S. pneumoniae protein sequence, SEQ ID 4691.
 PN US6800744-B1.
 PD 05-OCT-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 81.5; DB 8; Length 208;
 Best Local Similarity 20.2%; Pred. No. 2.4;
 RESULT 1459
 ID AEA59926 standard; protein; 208 AA.
 DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:4691.
 PN US2005136404-A1.
 PD 23-JUN-2005.
 PA (DOUC/) DOUCETTE-STAMM L A.
 PA (BUSH/) BUSH D.
 Query Match 5.9%; Score 81.5; DB 9; Length 208;
 Best Local Similarity 20.2%; Pred. No. 2.4;
 RESULT 1460
 ID ABU41035 standard; protein; 278 AA.
 DE Protein encoded by Prokaryotic essential gene #26562.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 81.5; DB 6; Length 278;
 Best Local Similarity 21.0%; Pred. No. 3.5;
 RESULT 1461
 ID ADF05890 standard; protein; 280 AA.
 DE Bacterial polypeptide #2003.
 PN US6605709-B1.
 PD 12-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 81.5; DB 7; Length 280;
 Best Local Similarity 21.0%; Pred. No. 3.6;
 RESULT 1462
 ID ADV10132 standard; protein; 332 AA.
 DE Plant full length insert polypeptide seqid 65947.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Query Match 5.9%; Score 81.5; DB 8; Length 332;

Best Local Similarity 21.8%; Pred. No. 4.5;
 RESULT 1463
 ID ABB91156 standard; protein; 351 AA.
 DE Herbicidally active polypeptide SEQ ID NO 367.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match 5.9%; Score 81.5; DB 5; Length 351;
 Best Local Similarity 23.1%; Pred. No. 4.9;
 RESULT 1464
 ID AAM93355 standard; protein; 399 AA.
 DE Human polypeptide, SEQ ID NO: 2909.
 PN EPI130094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 5.9%; Score 81.5; DB 4; Length 399;
 Best Local Similarity 22.6%; Pred. No. 5.8;
 RESULT 1465
 ID ADL30876 standard; protein; 399 AA.
 DE Human protein encoded by a full length cDNA clone SeqID 2909.
 PN EPI396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 5.9%; Score 81.5; DB 8; Length 399;
 Best Local Similarity 22.6%; Pred. No. 5.8;
 RESULT 1466
 ID ABU39717 standard; protein; 425 AA.
 DE Protein encoded by Prokaryotic essential gene #25244.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 81.5; DB 6; Length 425;
 Best Local Similarity 19.6%; Pred. No. 6.3;
 RESULT 1467
 ID AU33707 standard; protein; 438 AA.
 DE Pseudomonas aeruginosa cellular proliferation protein #151.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 81.5; DB 4; Length 438;
 Best Local Similarity 20.3%; Pred. No. 6.6;
 RESULT 1468
 ID ABU15537 standard; protein; 438 AA.
 DE Protein encoded by Prokaryotic essential gene #1124.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 81.5; DB 6; Length 438;
 Best Local Similarity 20.3%; Pred. No. 6.6;
 RESULT 1469
 ID ABO83917 standard; protein; 503 AA.
 DE Pseudomonas aeruginosa polypeptide #16092.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 81.5; DB 7; Length 503;
 Best Local Similarity 20.3%; Pred. No. 8;
 RESULT 1470
 ID ABP65039 standard; protein; 234 AA.
 DE Mouse membrane spanning 4-domain family, subfamily A 7 protein.
 PN WO200262946-A2.
 PD 15-AUG-2002.
 PA (UYDU-) UNIV DUKE.
 Query Match 5.8%; Score 81; DB 5; Length 234;
 Best Local Similarity 20.6%; Pred. No. 3.2;
 RESULT 1471
 ID ADD43824 standard; protein; 293 AA.
 DE Chlamydia trachomatis immunogenic protein, SEQ ID No 119.
 PN WO2003049762-A2.
 PD 19-JUN-2003.
 PA (CHIR-) CHIRON SPA.
 Query Match 5.8%; Score 81; DB 7; Length 293;
 Best Local Similarity 18.4%; Pred. No. 4.3;

RESULT 1472
ID AEA19116 standard; protein; 293 AA.
DE Chlamydia trachomatis protein - SEQ ID 119.
PN US2005106162-A1.
PD 19-MAY-2005.
PA (GRAN/) GRANDI G.
PA (RATT/) RATTI G.
Query Match 5.8%; Score 81; DB 9; Length 293;
Best Local Similarity 18.4%; Pred. No. 4.3;
RESULT 1473
ID ADA34894 standard; protein; 323 AA.
DE Acinetobacter baumannii protein #2055.
PN US562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 81; DB 6; Length 323;
Best Local Similarity 22.5%; Pred. No. 4.9;
RESULT 1474
ID AAO20532 standard; protein; 392 AA.
DE Protein of the human TFM-2 gene sequence.
PN WO200229041-A2.1
PD 11-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 81; DB 5; Length 392;
Best Local Similarity 17.8%; Pred. No. 6.4;
RESULT 1475
ID ADD37455 standard; protein; 394 AA.
DE Human transporter TFM-2.
PN US2003143675-A1.
PD 31-JUL-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 81; DB 7; Length 394;
Best Local Similarity 17.8%; Pred. No. 6.5;
RESULT 1476
ID ABO61692 standard; protein; 425 AA.
DE Klebsiella pneumoniae polypeptide seqid 8209.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 81; DB 7; Length 425;
Best Local Similarity 22.7%; Pred. No. 7.2;
RESULT 1477
ID AAE21184 standard; protein; 515 AA.
DE Human TRICH-28 protein.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INGV-) INCYTE GENOMICS INC.
Query Match 5.8%; Score 81; DB 5; Length 515;
Best Local Similarity 17.8%; Pred. No. 9.4;
RESULT 1478
ID ABJ37907 standard; protein; 515 AA.
DE NOVX protein sequence SEQ ID No 60.
PN WO200281517-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 81; DB 6; Length 515;
Best Local Similarity 17.8%; Pred. No. 9.4;
RESULT 1479
ID ADQ66916 standard; protein; 515 AA.
DE Novel human protein sequence #1889.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 81; DB 8; Length 515;
Best Local Similarity 17.8%; Pred. No. 9.4;
RESULT 1480
ID ABO84581 standard; protein; 515 AA.
DE Human cancer-associated protein HPI7-001.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.8%; Score 81; DB 8; Length 515;
Best Local Similarity 17.8%; Pred. No. 9.4;

RESULT 1481
ID ADH58563 standard; protein; 516 AA.
DE Human Na+-independent transporter-related transporter protein.
PN WO2003076644-A2.
PD 18-SEP-2003.
PA (APPL-) APPLERA CORP.
Query Match 5.8%; Score 81; DB 7; Length 516;
Best Local Similarity 17.8%; Pred. No. 9.4;
RESULT 1482
ID ADN23220 standard; protein; 544 AA.
DE Bacterial polypeptide #5873.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 81; DB 8; Length 544;
Best Local Similarity 23.0%; Pred. No. 10;
RESULT 1483
ID ABB64860 standard; protein; 875 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21372.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 81; DB 4; Length 875;
Best Local Similarity 20.9%; Pred. No. 19;
RESULT 1484
ID ABU39716 standard; protein; 1102 AA.
DE Protein encoded by Prokaryotic essential gene #25243.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 81; DB 6; Length 1102;
Best Local Similarity 20.0%; Pred. No. 27;
RESULT 1485
ID ADY52908 standard; protein; 260 AA.
DE Nodularia spumigena ketocarotenoid-related ketolase protein - SEQ ID 4.
PN WO2005019461-A2.
PD 03-MAR-2005.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.8%; Score 80.5; DB 9; Length 260;
Best Local Similarity 21.1%; Pred. No. 4.2;
RESULT 1486
ID ADY52974 standard; protein; 264 AA.
DE Nodularia spumigena ketocarotenoid-related ketolase protein - SEQ ID 70.
PN WO2005019461-A2.
PD 03-MAR-2005.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 5.8%; Score 80.5; DB 9; Length 264;
Best Local Similarity 21.1%; Pred. No. 4.3;
RESULT 1487
ID ABO65403 standard; protein; 298 AA.
DE Klebsiella pneumoniae polypeptide seqid 11920.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 80.5; DB 7; Length 298;
Best Local Similarity 18.5%; Pred. No. 5;
RESULT 1488
ID ABB32477 standard; protein; 359 AA.
DE Staphylococcus aureus polypeptide SEQ ID NO 14.
PN WO200177365-A2.
PD 18-OCT-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 80.5; DB 5; Length 359;
Best Local Similarity 23.4%; Pred. No. 6.5;
RESULT 1489
ID ABM72555 standard; protein; 359 AA.
DE Staphylococcus aureus protein #1795.
PN WO200294868-A2.
PD 28-NOV-2002.

PA (CHIR-) CHIRON SPA.
 Query Match 5.8%; Score 80.5; DB 6; Length 359;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1490
 ID ADC21330 standard; protein; 359 AA.
 DE Staphylococcus aureus protein SEQ ID NO: 12.
 PN W02003029484-A2.
 PD 10-APR-2003.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 5.8%; Score 80.5; DB 7; Length 359;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1491
 ID ADC25016 standard; protein; 359 AA.
 DE S. aureus polypeptide #6.
 PN US2003087321-A1.
 PD 08-MAY-2003.
 PA (TOMI/) TOMICH C C.
 PA (QUIN/) QUINN C L.
 PA (ARVI/) ARVIDSON S.
 PA (MOTT/) MOTT J E.
 PA (HARR/) HARRIS B W.
 Query Match 5.8%; Score 80.5; DB 7; Length 359;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1492
 ID ADD52518 standard; protein; 359 AA.
 DE Staphylococcus aureus unknown protein #6.
 PN US2003180821-A1.
 PD 25-SEP-2003.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 5.8%; Score 80.5; DB 7; Length 359;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1493
 ID ABB32489 standard; protein; 370 AA.
 DE Staphylococcus aureus polypeptide SEQ ID NO 74.
 PN W0200177365-A2.
 PD 18-OCT-2001.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 5.8%; Score 80.5; DB 5; Length 370;
 Best Local Similarity 23.4%; Pred. No. 6.8;
 RESULT 1494
 ID ADC21396 standard; protein; 370 AA.
 DE Staphylococcus aureus protein SEQ ID NO: 78.
 PN W02003029484-A2.
 PD 10-APR-2003.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 5.8%; Score 80.5; DB 7; Length 370;
 Best Local Similarity 23.4%; Pred. No. 6.8;
 RESULT 1495
 ID ADC25082 standard; protein; 370 AA.
 DE S. aureus polypeptide #6 encoded by the essential coding region.
 PN US2003087321-A1.
 PD 08-MAY-2003.
 PA (TOMI/) TOMICH C C.
 PA (QUIN/) QUINN C L.
 PA (ARVI/) ARVIDSON S.
 PA (MOTT/) MOTT J E.
 PA (HARR/) HARRIS D W.
 Query Match 5.8%; Score 80.5; DB 7; Length 370;
 Best Local Similarity 23.4%; Pred. No. 6.8;
 RESULT 1496
 ID ADD52584 standard; protein; 370 AA.
 DE Staphylococcus aureus essential protein #22.
 PN US2003180821-A1.
 PD 25-SEP-2003.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 Query Match 5.8%; Score 80.5; DB 7; Length 370;
 Best Local Similarity 23.4%; Pred. No. 6.8;
 RESULT 1497
 ID ABP38454 standard; protein; 411 AA.
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3299.
 PN US6380370-B1.
 PD 30-APR-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 5.8%; Score 80.5; DB 5; Length 411;
 Best Local Similarity 22.0%; Pred. No. 7.8;
 RESULT 1498
 ID ADS07146 standard; protein; 411 AA.
 DE Staphylococcus epidermis polypeptide seqid 6441.
 PN US2004147734-A1.
 PD 29-JUL-2004.
 PA (DOUC/) DOUCETTE-STAMM L.
 PA (BUSH/) BUSH D.
 Query Match 5.8%; Score 80.5; DB 8; Length 411;
 Best Local Similarity 22.0%; Pred. No. 7.8;
 RESULT 1499
 ID ABU41976 standard; protein; 438 AA.
 DE Protein encoded by Prokaryotic essential gene #27503.
 PN W0200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.8%; Score 80.5; DB 6; Length 438;
 Best Local Similarity 18.7%; Pred. No. 8.5;
 RESULT 1500
 ID ADC77508 standard; protein; 458 AA.
 DE Zebrafish TDE1 protein SEQ ID NO:3.
 PN W02003066829-A2.
 PD 14-AUG-2003.
 PA (DISC-) DISCOVERY GENOMICS INC.
 Query Match 5.8%; Score 80.5; DB 7; Length 458;
 Best Local Similarity 23.3%; Pred. No. 9.1;

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 7, 2006, 16:36:52 ; Search time 48 Seconds
(without alignments)
458.161 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392

Sequence: 1 MMWFOGLSFLPSALVWTS.....YDTPACPINNERTLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/aaa/5.COMB.pep.*

2: /cgn2_6/prodata/1/aaa/6.COMB.pep.*

3: /cgn2_6/prodata/1/aaa/H.COMB.pep.*

4: /cgn2_6/prodata/1/aaa/PCTUS.COMB.pep.*

5: /cgn2_6/prodata/1/aaa/RE.COMB.pep.*

6: /cgn2_6/prodata/1/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1392	100.0	266	2	US-09-991-181-23
2	1392	100.0	266	2	US-09-990-444-23
3	1392	100.0	266	2	US-09-997-333-23
4	1392	100.0	266	2	US-09-992-598-23
5	1388	99.7	267	2	US-09-663-600A-190
6	595.5	42.8	172	2	US-09-663-600A-96
7	479.5	34.4	238	2	US-09-724-864-38
8	358	25.7	69	2	US-09-663-600A-130
9	358	25.7	69	2	US-09-663-600A-224
10	118	8.5	21	2	US-08-905-223-20
11	118	8.5	21	2	US-09-247-155-20
12	118	8.5	21	2	US-09-663-600A-20
13	118	8.5	21	2	US-09-621-976-2
14	118	8.5	21	2	US-09-513-999C-2
15	118	8.5	21	2	US-09-471-276-2
16	118	8.5	21	2	US-09-903-190-20
17	91.5	6.6	291	2	US-09-107-532A-4147
18	91.5	6.6	387	2	US-09-721-870-14
19	90	6.5	283	2	US-09-602-787A-588
20	90	6.5	396	2	US-09-248-796A-20434
21	88	6.3	344	2	US-09-248-796A-16383
22	88	6.3	1165	1	US-08-240-357-2
23	86.5	6.2	356	2	US-09-134-000C-4914
24	85.5	6.1	579	2	US-09-786-681A-4
25	85.5	6.1	582	2	US-09-786-681A-2
26	85	6.1	419	2	US-09-948-774-2
27	85	6.1	1180	2	US-08-726-214-12
28	84.5	6.1	28	28	US-09-134-000C-6205
29	84.5	6.1	29	29	US-10-144-929-114
30	84.5	6.1	30	30	US-09-991-181-73
31	84.5	6.1	31	31	US-09-990-444-73
32	84.5	6.1	32	32	US-09-997-333-73
33	84.5	6.1	33	33	US-09-992-598-73
34	84	6.0	241	2	US-09-328-352-8001
35	84	6.0	36	36	US-09-540-236-2605
36	84	6.0	37	37	US-09-489-039A-14149
37	84	6.0	38	38	US-09-252-991A-22527
38	84	6.0	39	39	US-09-252-991A-19581
39	84	6.0	40	40	US-09-489-039A-13574
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103	77.5	5.6	287	2	US-09-543-681A-5282	Sequence 5282, Ap	176	74	5.3	448	2	US-09-543-681A-7245	Sequence 7245, Ap
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108	77	5.5	385	2	US-09-540-236-3736	Sequence 3736, Ap	181	73.5	5.3	297	2	US-09-489-039A-8466	Sequence 8466, Ap
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112	76.5	5.5	483	2	US-09-710-279-3132	Sequence 3132, Ap	185	73.5	5.3	391	1	US-08-103-445-5	Sequence 5, Appli
113	76.5	5.5	568	2	US-09-949-016-6719	Sequence 6719, Ap	186	73.5	5.3	391	1	US-08-461-690B-5	Sequence 5, Appli
114	76.5	5.5	596	2	US-09-949-016-8124	Sequence 8124, Ap	187	73.5	5.3	391	1	US-08-501-003A-16	Sequence 16, Appl
115	76.5	5.5	630	2	US-09-134-001C-4615	Sequence 4615, Ap	188	73.5	5.3	391	2	US-09-543-681A-8292	Sequence 8292, Ap
116	76	5.5	320	2	US-09-543-681A-7972	Sequence 7972, Ap	189	73.5	5.3	391	2	US-09-275-252A-13	Sequence 13, Appl
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121	76	5.5	429	2	US-09-922-501-10	Sequence 10, Appl	194	73.5	5.3	428	2	US-09-438-185A-682	Sequence 682, App
122	76	5.5	435	6	5268463-9	Patent No. 5268463	195	73.5	5.3	514	2	US-09-489-039A-11902	Sequence 11902, A
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127	75.5	5.4	445	2	US-09-328-352-6669	Sequence 6669, Ap	200	73.5	5.3	717	2	US-08-726-214-14	Sequence 14, Appl
128	75.5	5.4	517	2	US-09-248-796A-20437	Sequence 20437, A	201	73.5	5.3	1099	2	US-08-134-000C-5833	Sequence 5833, Ap
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131	75.5	5.4	1172	2	US-09-328-352-6071	Sequence 6071, Ap	204	73.5	5.3	2485	4	PCT-US94-00198-2	Sequence 2, Appli
132	75	5.4	218	2	US-09-328-352-5215	Sequence 5215, Ap	205	73.5	5.3	2818	1	US-08-510-284-1	Sequence 1, Appli
133	75	5.4	283	2	US-09-107-433-3024	Sequence 3024, Ap	206	73.5	5.3	2818	1	US-08-411-389-2	Sequence 2, Appli
134	75	5.4	290	2	US-09-134-001C-4893	Sequence 4893, Ap	207	73.5	5.3	2818	1	US-08-449-933-2	Sequence 2, Appli
135	75	5.4	344	1	US-08-689-974-1	Sequence 1, Appli	208	73.5	5.3	2818	2	US-07-966-049A-2	Sequence 2, Appli
136	75	5.4	344	2	US-09-058-376-1	Sequence 4, Appli	209	73.5	5.3	2818	2	US-09-542-331-2	Sequence 2, Appli
137	75	5.4	394	2	US-09-144-914-4	Sequence 4, Appli	210	73.5	5.3	2818	2	US-09-510-791-2	Sequence 2, Appli
138	75	5.4	394	2	US-09-655-272-5	Sequence 5, Appli	211	73	5.2	178	2	US-09-328-352-5593	Sequence 5593, Ap
139	75	5.4	399	2	US-09-489-039A-9414	Sequence 9414, Ap	212	73	5.2	187	2	US-09-328-352-7918	Sequence 7918, Ap
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151	74.5	5.4	367	2	US-09-438-185A-996	Sequence 996, App	224	72.5	5.2	389	2	US-09-328-352-5055	Sequence 5055, Ap
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154	74.5	5.4	405	2	US-09-719-088B-3	Sequence 3, Appli	227	72.5	5.2	519	2	US-09-248-796A-20368	Sequence 20368, A
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157	74.5	5.4	443	2	US-09-328-352-7069	Sequence 7069, Ap	230	72	5.2	273	2	US-09-328-352-5843	Sequence 5843, Ap
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161	74.5	5.4	824	2	US-09-605-703B-358	Sequence 358, App	234	72	5.2	430	2	US-09-134-001C-2981	Sequence 2981, Ap
162	74.5	5.4	832	2	US-09-605-703B-356	Sequence 356, App	235	72	5.2	468	2	US-09-543-681A-4671	Sequence 4671, Ap
163	74.5	5.4	1798	2	US-09-270-767-60233	Sequence 60233, A	236	72	5.2	495	2	US-09-359-167-4	Sequence 4, Appli
164	74.5	5.4	2410	2	US-09-270-767-60233	Sequence 44775, A	237	72	5.2	502	2	US-09-579-250-12	Sequence 12, Appl
165	74	5.3	173	2	US-09-252-991A-22033	Sequence 22033, A	238	72	5.2	502	2	US-09-579-250-14	Sequence 14, Appl
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171	74	5.3	292	2	US-09-348-116A-2	Sequence 2, Appli	244	72	5.2	906	2	US-08-473-089-31	Sequence 31, Appl
172	74	5.3	307	2	US-09-303-518D-408	Sequence 408, App	245	72	5.2	906	2	US-08-487-072A-31	Sequence 31, Appl
173	74	5.3	332	2	US-09-902-540-15291	Sequence 15291, A	246	71.5	5.1	228	2	US-09-973-278-160	Sequence 160, App

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248	71.5	237	1	US-08-818-514-3	Sequence 3, Appli	321	71	5.1	918	2	US-09-853-180B-3	Sequence 3, Appli
249	71.5	237	2	US-09-115-934A-3	Sequence 3, Appli	322	71	5.1	918	2	US-09-949-002-333	Sequence 333, App
250	71.5	237	2	US-09-611-175-3	Sequence 3, Appli	323	71	5.1	922	2	US-09-569-611C-41	Sequence 41, Appli
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252	71.5	287	2	US-09-134-001C-5055	Sequence 5055, App	325	71	5.1	951	2	US-10-282-163-9	Sequence 9, Appli
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257	71.5	339	1	US-08-501-003A-11	Sequence 11, Appl	330	70.5	5.1	319	2	US-09-130-749-2	Sequence 2, Appli
258	71.5	331	1	US-08-501-003A-13	Sequence 13, Appl	331	70.5	5.1	319	2	US-09-170-496D-60	Sequence 60, Appl
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263	71.5	484	2	US-09-248-796A-20357	Sequence 20357, A	336	70.5	5.1	420	2	US-09-134-001C-3805	Sequence 3805, Ap
264	71.5	519	2	US-09-198-452A-561	Sequence 561, App	337	70.5	5.1	443	2	US-09-489-039A-8166	Sequence 8166, Ap
265	71.5	531	2	US-09-438-185A-523	Sequence 523, App	338	70.5	5.1	444	2	US-09-328-352-5249	Sequence 5249, Ap
266	71.5	535	2	US-09-252-991A-21652	Sequence 21652, A	339	70.5	5.1	454	1	US-08-748-485-1	Sequence 1, Appli
267	71.5	552	2	US-09-270-767-45540	Sequence 45540, A	340	70.5	5.1	467	2	US-09-107-532A-6175	Sequence 6175, Ap
268	71.5	574	2	US-09-248-796A-20132	Sequence 20132, A	341	70.5	5.1	472	2	US-09-934-899-10	Sequence 10, Appl
269	71.5	587	2	US-08-635-552A-3	Sequence 3, Appli	342	70.5	5.1	472	2	US-09-934-868-30	Sequence 30, Appl
270	71	201	2	US-09-270-767-33463	Sequence 33463, A	343	70.5	5.1	472	2	US-10-701-200-30	Sequence 30, Appl
271	71	281	2	US-09-270-767-48680	Sequence 48680, A	344	70.5	5.1	473	2	US-09-949-016-11735	Sequence 11735, A
272	71	261	2	US-10-012-231A-326	Sequence 326, App	345	70.5	5.1	474	2	US-09-486-192-4	Sequence 4, Appli
273	71	261	2	US-10-015-389A-326	Sequence 326, App	346	70.5	5.1	474	2	US-10-328-459A-4	Sequence 4, Appli
274	71	261	2	US-10-006-768A-326	Sequence 326, App	347	70.5	5.1	500	2	US-09-489-039A-10995	Sequence 10995, A
275	71	261	2	US-10-015-671A-326	Sequence 326, App	348	70.5	5.1	619	2	US-09-248-796A-20837	Sequence 20837, A
276	71	261	2	US-10-015-393A-326	Sequence 326, App	349	70.5	5.1	669	2	US-09-949-016-6720	Sequence 6720, Ap
277	71	261	2	US-10-011-833A-326	Sequence 326, App	350	70.5	5.1	681	2	US-09-248-796A-20121	Sequence 20121, A
278	71	261	2	US-10-006-041A-326	Sequence 326, App	351	70.5	5.1	877	1	US-08-072-574-12	Sequence 12, Appl
279	71	261	2	US-10-012-064A-326	Sequence 326, App	352	70.5	5.1	955	2	US-09-252-991A-18882	Sequence 18882, A
280	71	332	2	US-09-313-942-10	Sequence 10, Appl	353	70.5	5.1	1134	2	US-08-726-214-2	Sequence 2, Appli
281	71	332	2	US-10-282-162-10	Sequence 10, Appl	354	70.5	5.1	1134	2	US-09-245-039-2	Sequence 2, Appli
282	71	347	2	US-09-769-787-20	Sequence 20, Appl	355	70.5	5.1	1681	2	US-09-920-653B-3	Sequence 3, Appli
283	71	369	2	US-09-838-955A-3	Sequence 3, Appli	356	70.5	5.1	1788	1	US-08-962-284-2	Sequence 2, Appli
284	71	384	2	US-09-902-540-11956	Sequence 11956, A	357	70	5.0	139	2	US-09-489-039A-8585	Sequence 8585, Ap
285	71	388	2	US-09-222-938A-37	Sequence 37, Appl	358	70	5.0	235	2	US-09-252-991A-19945	Sequence 19945, A
286	71	397	2	US-09-583-110-2946	Sequence 2946, Ap	359	70	5.0	296	2	US-09-328-352-7482	Sequence 7482, Ap
287	71	404	2	US-09-107-433-3747	Sequence 3747, Ap	360	70	5.0	314	2	US-09-543-681A-6497	Sequence 6497, Ap
288	71	408	2	US-09-489-039A-9583	Sequence 9583, Ap	361	70	5.0	429	2	US-09-156-809-1	Sequence 1, Appli
289	71	454	2	US-09-489-847-305	Sequence 305, App	362	70	5.0	429	2	US-10-006-915-1	Sequence 1, Appli
290	71	461	2	US-09-043-944-1	Sequence 1, Appli	363	70	5.0	492	2	US-09-328-352-6875	Sequence 6875, Ap
291	71	461	2	US-09-043-944-6	Sequence 6, Appli	364	70	5.0	496	2	US-09-489-039A-8772	Sequence 8772, Ap
292	71	461	2	US-10-811-199-1	Sequence 1, Appli	365	70	5.0	502	2	US-08-771-737-2	Sequence 2, Appli
293	71	461	2	US-10-811-199-6	Sequence 6, Appli	366	70	5.0	502	2	US-09-954-936-2	Sequence 2, Appli
294	71	465	2	US-09-710-279-1676	Sequence 1676, Ap	367	70	5.0	526	2	US-09-543-681A-6494	Sequence 6494, Ap
295	71	466	2	US-09-328-352-7117	Sequence 7117, Ap	368	70	5.0	535	2	US-09-252-991A-21805	Sequence 21805, A
296	71	502	1	US-08-278-635B-7	Sequence 7, Appli	369	70	5.0	539	2	US-09-538-092-741	Sequence 741, App
297	71	502	1	US-08-466-589-8	Sequence 8, Appli	370	70	5.0	560	2	US-09-999-833A-420	Sequence 420, App
298	71	502	2	US-08-700-636-8	Sequence 8, Appli	371	70	5.0	560	2	US-10-020-445A-420	Sequence 420, App
299	71	502	2	US-08-464-258B-7	Sequence 7, Appli	372	70	5.0	594	2	US-09-489-039A-10622	Sequence 10622, A
300	71	502	2	US-08-467-574-8	Sequence 8, Appli	373	70	5.0	688	2	US-09-438-185A-870	Sequence 870, App
301	71	502	2	US-08-471-961-7	Sequence 7, Appli	374	70	5.0	708	1	US-07-797-556-2	Sequence 2, Appli
302	71	502	2	US-09-217-345-8	Sequence 8, Appli	375	70	5.0	708	1	US-08-308-881-2	Sequence 2, Appli
303	71	502	2	US-08-487-596-12	Sequence 12, Appl	376	70	5.0	708	1	US-09-058-263-2	Sequence 2, Appli
304	71	502	2	US-09-345-109C-7	Sequence 7, Appli	377	70	5.0	708	1	US-09-059-099-2	Sequence 2, Appli
305	71	502	2	US-09-892-985-8	Sequence 8, Appli	378	70	5.0	708	2	US-09-058-264-2	Sequence 2, Appli
306	71	502	2	US-09-579-250-2	Sequence 2, Appli	379	70	5.0	708	2	US-09-455-963-2	Sequence 2, Appli
307	71	502	2	US-09-579-250-10	Sequence 10, Appl	380	70	5.0	708	4	PCT-US95-06530-2	Sequence 2, Appli
308	71	502	2	US-09-703-951A-12	Sequence 12, Appl	381	70	5.0	1028	2	US-09-328-352-5749	Sequence 5749, Ap
309	71	571	2	US-09-252-991A-28549	Sequence 28549, A	382	70	5.0	1165	2	US-09-949-016-6874	Sequence 6874, Ap
310	71	594	2	US-09-650-324A-59	Sequence 59, Appl	383	70	5.0	1165	2	US-09-949-016-11392	Sequence 11392, A
311	71	594	2	US-10-039-112A-59	Sequence 59, Appl	384	70	5.0	2105	1	US-08-808-793-3	Sequence 3, Appli
312	71	627	2	US-09-902-540-15743	Sequence 15743, A	385	70	5.0	2105	2	US-08-772-512A-3	Sequence 3, Appli
313	71	658	1	US-08-825-558-4	Sequence 4, Appli	386	70	5.0	2105	2	US-09-428-371-3	Sequence 3, Appli
314	71	658	2	US-09-312-611-4	Sequence 4, Appli	387	69.5	5.0	293	2	US-09-902-540-11200	Sequence 11200, A
315	71	693	2	US-09-999-833A-483	Sequence 483, App	388	69.5	5.0	308	2	US-09-595-386-3	Sequence 3, Appli
316	71	693	2	US-10-020-445A-483	Sequence 483, App	389	69.5	5.0	308	2	US-09-993-525-3	Sequence 3, Appli
317	71	859	2	US-09-313-942-7	Sequence 7, Appli	390	69.5	5.0	345	2	US-09-543-681A-7546	Sequence 7546, Ap
318	71	859	2	US-10-282-162-7	Sequence 7, Appli	391	69.5	5.0	350	2	US-09-540-236-2338	Sequence 2338, Ap
319	71	918	1	US-08-825-558-6	Sequence 6, Appli	392	69.5	5.0	406	2	US-09-328-352-7149	Sequence 7149, Ap

393	69.5	5.0	417	2	US-09-405-558-44	Sequence 44, Appl	466	68.5	4.9	405	2	US-09-543-681A-6109	Sequence 6109, Ap
394	69.5	5.0	417	2	US-09-538-036-44	Sequence 44, Appl	467	68.5	4.9	412	2	US-09-134-001C-4885	Sequence 4885, Ap
395	69.5	5.0	456	2	US-09-489-039A-8332	Sequence 8332, Ap	468	68.5	4.9	427	2	US-09-252-991A-29948	Sequence 29948, A
396	69.5	5.0	460	2	US-09-489-039A-13505	Sequence 13505, A	469	68.5	4.9	428	2	US-09-328-352-5543	Sequence 5543, Ap
397	69.5	5.0	493	1	US-08-362-512A-4	Sequence 4, Appl	470	68.5	4.9	459	2	US-09-583-110-5017	Sequence 5017, Ap
398	69.5	5.0	493	2	US-08-964-933A-4	Sequence 4, Appl	471	68.5	4.9	459	2	US-09-769-787-85	Sequence 85, Appl
399	69.5	5.0	493	2	US-09-854-774-4	Sequence 4, Appl	472	68.5	4.9	465	2	US-09-489-039A-7435	Sequence 7435, Ap
400	69.5	5.0	501	2	US-09-252-991A-28456	Sequence 28456, A	473	68.5	4.9	470	2	US-09-107-433-4341	Sequence 4341, Ap
401	69.5	5.0	513	1	US-09-122-230-7	Sequence 7, Appl	474	68.5	4.9	480	2	US-09-305-681-2	Sequence 2, Appl
402	69.5	5.0	530	2	US-09-540-236-2483	Sequence 2483, Ap	475	68.5	4.9	487	2	US-09-911-132A-4	Sequence 4, Appl
403	69.5	5.0	591	2	US-09-643-657-15	Sequence 15, Appl	476	68.5	4.9	511	2	US-09-305-681-6	Sequence 6, Appl
404	69.5	5.0	627	2	US-09-538-092-760	Sequence 760, Ap	477	68.5	4.9	538	2	US-09-252-991A-23060	Sequence 23060, A
405	69.5	5.0	653	1	US-07-782-298-2	Sequence 2, Appl	478	68.5	4.9	541	2	US-09-976-594-931	Sequence 931, App
406	69.5	5.0	688	2	US-09-543-681A-4896	Sequence 4896, Ap	479	68.5	4.9	549	2	US-09-248-796A-20436	Sequence 20436, A
407	69.5	5.0	1277	2	US-09-397-885-3	Sequence 3, Appl	480	68.5	4.9	716	2	US-09-303-518D-108	Sequence 108, App
408	69.5	5.0	1277	2	US-09-969-362-3	Sequence 3, Appl	481	68.5	4.9	1091	2	US-09-306-595C-7	Sequence 7, Appl
409	69	5.0	114	2	US-09-134-001C-3376	Sequence 3376, Ap	482	68.5	4.9	1091	2	US-09-925-388-7	Sequence 7, Appl
410	69	5.0	201	2	US-09-605-703B-1952	Sequence 1952, Ap	483	68.5	4.9	1091	2	US-10-431-846-7	Sequence 7, Appl
411	69	5.0	241	2	US-09-328-352-7032	Sequence 7032, Ap	484	68.5	4.9	2104	1	US-08-808-793-4	Sequence 4, Appl
412	69	5.0	292	2	US-09-270-767-41753	Sequence 41753, A	485	68.5	4.9	2104	2	US-08-772-512A-4	Sequence 4, Appl
413	69	5.0	293	2	US-09-438-185A-313	Sequence 313, App	486	68.5	4.9	2104	2	US-09-428-371-4	Sequence 4, Appl
414	69	5.0	294	2	US-09-902-540-11124	Sequence 11124, A	487	68.5	4.9	3559	2	US-09-693-205A-10	Sequence 10, Appl
415	69	5.0	307	2	US-09-605-703B-2582	Sequence 2582, Ap	488	68	4.9	253	2	US-08-858-207A-299	Sequence 299, App
416	69	5.0	308	2	US-09-198-452A-606	Sequence 606, App	489	68	4.9	279	2	US-09-602-787A-658	Sequence 658, App
417	69	5.0	308	2	US-09-438-185A-569	Sequence 569, App	490	68	4.9	309	2	US-09-710-279-42	Sequence 42, Appl
418	69	5.0	316	1	US-08-827-291A-2	Sequence 2, Appl	491	68	4.9	313	2	US-09-583-110-4236	Sequence 4236, Ap
419	69	5.0	321	2	US-10-314-048A-10	Sequence 10, Appl	492	68	4.9	315	2	US-09-107-433-3706	Sequence 3706, Ap
420	69	5.0	344	2	US-10-121-757B-20	Sequence 20, Appl	493	68	4.9	355	2	US-09-826-509-475	Sequence 475, App
421	69	5.0	359	2	US-09-875-076-28	Sequence 28, Appl	494	68	4.9	379	2	US-09-252-991A-27854	Sequence 27854, A
422	69	5.0	380	1	US-08-227-108-16	Sequence 16, Appl	495	68	4.9	404	2	US-09-328-352-8182	Sequence 8182, A
423	69	5.0	380	1	US-09-073-674-16	Sequence 16, Appl	496	68	4.9	466	2	US-09-603-208A-236	Sequence 236, App
424	69	5.0	397	2	US-09-328-352-7357	Sequence 7357, Ap	497	68	4.9	470	2	US-09-328-352-6573	Sequence 6573, Ap
425	69	5.0	403	2	US-09-489-039A-9921	Sequence 9921, Ap	498	68	4.9	476	2	US-09-328-352-6735	Sequence 6735, Ap
426	69	5.0	420	2	US-09-328-352-5907	Sequence 5907, Ap	499	68	4.9	484	2	US-09-134-001C-5063	Sequence 5063, Ap
427	69	5.0	446	2	US-09-248-796A-20349	Sequence 20349, A	500	68	4.9	486	2	US-09-134-001C-3593	Sequence 3593, Ap
428	69	5.0	451	2	US-09-303-518D-150	Sequence 150, App	501	68	4.9	503	2	US-09-248-796A-16650	Sequence 16650, A
429	69	5.0	451	2	US-09-303-518D-152	Sequence 152, App	502	68	4.9	548	2	US-09-328-352-6605	Sequence 6605, Ap
430	69	5.0	483	2	US-09-134-000C-4234	Sequence 4234, Ap	503	68	4.9	605	2	US-09-583-110-4773	Sequence 4773, Ap
431	69	5.0	506	2	US-09-540-236-2360	Sequence 2360, Ap	504	68	4.9	619	2	US-09-540-236-2377	Sequence 2377, Ap
432	69	5.0	520	2	US-09-248-796A-20803	Sequence 20803, A	505	68	4.9	633	2	US-09-328-352-5439	Sequence 5439, Ap
433	69	5.0	583	2	US-09-489-039A-13918	Sequence 13918, A	506	68	4.9	638	1	US-08-295-814E-13	Sequence 13, Appl
434	69	5.0	642	2	US-09-252-991A-23588	Sequence 23588, A	507	68	4.9	638	1	US-08-240-783B-2	Sequence 2, Appl
435	69	5.0	719	2	US-09-328-352-6274	Sequence 6274, Ap	508	68	4.9	638	2	US-09-084-813-2	Sequence 2, Appl
436	69	5.0	852	2	US-09-254-344-4	Sequence 4, Appl	509	68	4.9	638	2	US-09-343-361-13	Sequence 13, Appl
437	69	5.0	854	2	US-09-254-352B-18	Sequence 18, Appl	510	68	4.9	638	4	PCT-US92-09862-2	Sequence 2, Appl
438	69	5.0	934	1	US-08-215-805A-80	Sequence 80, Appl	511	68	4.9	640	2	US-09-627-376-16	Sequence 16, Appl
439	69	5.0	1035	2	US-09-112-096-15	Sequence 15, Appl	512	68	4.9	640	2	US-10-047-676B-16	Sequence 16, Appl
440	69	5.0	1095	2	US-09-636-215-778	Sequence 778, App	513	68	4.9	672	2	US-09-543-681A-5976	Sequence 5976, Ap
441	69	5.0	1095	2	US-09-685-166A-778	Sequence 778, App	514	68	4.9	694	2	US-09-248-796A-20210	Sequence 20210, A
442	69	5.0	1095	2	US-09-679-426-778	Sequence 778, App	515	68	4.9	727	2	US-09-543-681A-6690	Sequence 6690, Ap
443	69	5.0	1095	2	US-09-759-143-778	Sequence 778, App	516	68	4.9	783	2	US-09-165-396-2	Sequence 2, Appl
444	69	5.0	1095	2	US-09-651-236-778	Sequence 778, App	517	68	4.9	905	2	US-09-538-092-1079	Sequence 1079, Ap
445	69	5.0	1095	2	US-09-657-279-778	Sequence 778, App	518	68	4.9	1024	2	US-09-562-737-87	Sequence 87, Appl
446	69	5.0	1095	2	US-10-012-896-778	Sequence 778, App	519	68	4.9	2864	2	US-08-469-260A-394	Sequence 394, App
447	69	5.0	1180	1	US-08-072-574-8	Sequence 8, Appl	520	68	4.9	2864	2	US-08-488-446-394	Sequence 394, App
448	69	5.0	1212	1	US-08-072-574-10	Sequence 10, Appl	521	68	4.9	2864	2	US-08-467-344A-394	Sequence 394, App
449	69	5.0	2037	2	US-09-543-681A-5538	Sequence 5538, Ap	522	68	4.9	2864	2	US-08-424-550B-394	Sequence 394, App
450	69	5.0	2873	1	US-08-466-033-15	Sequence 15, Appl	523	67.5	4.8	181	2	US-09-270-767-33574	Sequence 33574, A
451	69	5.0	2873	1	US-08-638-911A-2	Sequence 2, Appl	524	67.5	4.8	196	2	US-09-383-586-11	Sequence 11, Appl
452	69	5.0	2873	1	US-08-444-733-15	Sequence 15, Appl	525	67.5	4.8	196	2	US-09-823-038A-11	Sequence 11, Appl
453	69	5.0	2873	1	US-08-464-134-15	Sequence 15, Appl	526	67.5	4.8	249	2	US-09-540-236-2487	Sequence 2487, Ap
454	69	5.0	2873	1	US-08-461-361-15	Sequence 15, Appl	527	67.5	4.8	249	2	US-09-949-016-7192	Sequence 7192, Ap
455	69	5.0	2873	1	US-08-485-910-15	Sequence 15, Appl	528	67.5	4.8	264	2	US-09-270-767-41787	Sequence 41787, A
456	69	5.0	2873	4	PCT-US95-06266-15	Sequence 15, Appl	529	67.5	4.8	265	2	US-09-248-796A-17984	Sequence 17984, A
457	68.5	4.9	180	2	US-09-270-767-32589	Sequence 32589, A	530	67.5	4.8	304	2	US-09-328-352-6103	Sequence 6103, Ap
458	68.5	4.9	180	2	US-09-270-767-47806	Sequence 47806, A	531	67.5	4.8	317	2	US-09-489-039A-9602	Sequence 9602, Ap
459	68.5	4.9	241	1	US-08-825-781-3	Sequence 3, Appl	532	67.5	4.8	323	2	US-09-107-532A-5460	Sequence 5460, Ap
460	68.5	4.9	264	2	US-09-724-864-64	Sequence 64, Appl	533	67.5	4.8	327	2	US-09-543-681A-6219	Sequence 6219, Ap
461	68.5	4.9	300	2	US-09-489-039A-10701	Sequence 10701, A	534	67.5	4.8	336	1	US-08-332-312-4	Sequence 4, Appl
462	68.5	4.9	346	2	US-10-152-886-91	Sequence 91, Appl	535	67.5	4.8	360	2	US-09-949-016-10048	Sequence 10048, A
463	68.5	4.9	365	2	US-09-902-540-14946	Sequence 14946, A	536	67.5	4.8	370	2	US-09-303-518D-110	Sequence 110, App
464	68.5	4.9	396	2	US-09-107-532A-4277	Sequence 4277, Ap	537	67.5	4.8	411	2	US-09-328-352-5039	Sequence 5039, Ap
465	68.5	4.9	400	2	US-09-134-001C-2912	Sequence 2912, Ap	538	67.5	4.8	421	2	US-09-198-452A-932	Sequence 932, App

539	67.5	4.8	421	2	US-09-438-185A-869	Sequence 869, App	612	66.5	4.8	249	2	US-08-858-207A-309	Sequence 309, App
540	67.5	4.8	422	2	US-09-134-000C-5971	Sequence 5971, Ap	613	66.5	4.8	249	2	US-09-270-767-38186	Sequence 38186, A
541	67.5	4.8	484	2	US-09-252-991A-33299	Sequence 33299, A	614	66.5	4.8	249	2	US-09-270-767-53403	Sequence 53403, A
542	67.5	4.8	536	2	US-09-107-532A-5507	Sequence 5507, Ap	615	66.5	4.8	256	2	US-09-489-039A-9057	Sequence 9057, Ap
543	67.5	4.8	586	2	US-09-252-991A-24994	Sequence 24994, A	616	66.5	4.8	274	2	US-09-830-230A-19	Sequence 19, App
544	67.5	4.8	632	2	US-09-248-796A-18040	Sequence 18040, A	617	66.5	4.8	300	2	US-09-393-634-19	Sequence 190, App
545	67.5	4.8	632	2	US-09-902-540-15330	Sequence 15330, A	618	66.5	4.8	306	2	US-09-830-230A-189	Sequence 189, App
546	67.5	4.8	632	2	US-09-949-016-10386	Sequence 10386, A	619	66.5	4.8	319	2	US-09-170-496D-136	Sequence 196, App
547	67.5	4.8	662	2	US-09-583-110-5119	Sequence 5119, Ap	620	66.5	4.8	324	2	US-09-543-681A-6241	Sequence 6241, Ap
548	67.5	4.8	664	2	US-09-107-433-2775	Sequence 2775, Ap	621	66.5	4.8	343	2	US-09-543-681A-6853	Sequence 6853, Ap
549	67.5	4.8	667	1	US-07-879-617A-8	Sequence 8, Appli	622	66.5	4.8	349	2	US-09-491-577-96	Sequence 96, Appli
550	67.5	4.8	667	1	US-08-753-985-8	Sequence 8, Appli	623	66.5	4.8	380	2	US-09-949-016-10856	Sequence 10856, A
551	67.5	4.8	680	2	US-09-720-317A-18	Sequence 18, Appli	624	66.5	4.8	392	2	US-09-603-208A-134	Sequence 134, App
552	67.5	4.8	693	2	US-09-949-016-9666	Sequence 9666, Ap	625	66.5	4.8	412	2	US-09-710-279-368	Sequence 368, App
553	67.5	4.8	716	2	US-09-303-518D-112	Sequence 112, App	626	66.5	4.8	414	2	US-09-605-703B-2352	Sequence 2352, Ap
554	67.5	4.8	767	2	US-09-328-352-4613	Sequence 4613, Ap	627	66.5	4.8	415	2	US-09-489-039A-10457	Sequence 10457, A
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556	67.5	4.8	912	2	US-09-641-318-2	Sequence 2, Appli	629	66.5	4.8	430	2	US-10-104-047-2285	Sequence 2285, Ap
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558	67.5	4.8	940	2	US-09-328-352-8165	Sequence 8165, Ap	631	66.5	4.8	456	2	US-09-328-352-5446	Sequence 5446, Ap
559	67.5	4.8	1084	2	US-09-221-013A-8	Sequence 8, Appli	632	66.5	4.8	470	1	US-08-959-011-1	Sequence 1, Appli
560	67.5	4.8	1326	2	US-09-328-352-4886	Sequence 4886, Ap	633	66.5	4.8	488	2	US-09-801-052-5	Sequence 5, Appli
561	67	4.8	148	2	US-09-270-767-39883	Sequence 39883, A	634	66.5	4.8	488	2	US-10-020-121-5	Sequence 5, Appli
562	67	4.8	148	2	US-09-270-767-55100	Sequence 55100, A	635	66.5	4.8	488	2	US-10-636-579-5	Sequence 9, Appli
563	67	4.8	162	2	US-09-270-767-45268	Sequence 45268, A	636	66.5	4.8	503	2	US-09-920-262A-9	Sequence 9, Appli
564	67	4.8	184	2	US-09-795-926-46	Sequence 46, Appli	637	66.5	4.8	511	2	US-09-328-352-6365	Sequence 6365, Ap
565	67	4.8	184	2	US-10-364-774-46	Sequence 46, Appli	638	66.5	4.8	515	2	US-09-489-039A-8402	Sequence 8402, Ap
566	67	4.8	205	2	US-09-252-991A-28363	Sequence 28363, A	639	66.5	4.8	525	2	US-09-252-991A-23870	Sequence 23870, A
567	67	4.8	217	2	US-09-134-000C-6287	Sequence 6287, Ap	640	66.5	4.8	534	2	US-09-107-532A-6592	Sequence 6592, Ap
568	67	4.8	225	2	US-09-543-681A-7698	Sequence 7698, Ap	641	66.5	4.8	535	2	US-09-107-532A-6593	Sequence 6593, Ap
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571	67	4.8	306	2	US-09-489-039A-10023	Sequence 10023, A	644	66.5	4.8	598	2	US-09-107-532A-7027	Sequence 7027, Ap
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573	67	4.8	335	2	US-08-248-796A-20118	Sequence 20118, A	646	66.5	4.8	670	2	US-09-107-433-4919	Sequence 4919, Ap
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575	67	4.8	360	2	US-09-489-039A-8125	Sequence 8125, Ap	648	66.5	4.8	688	2	US-09-720-317A-2	Sequence 2, Appli
576	67	4.8	375	2	US-09-543-681A-4465	Sequence 4465, Ap	649	66.5	4.8	719	2	US-09-438-185A-788	Sequence 788, App
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588	67	4.8	505	2	US-09-328-352-7155	Sequence 7155, Ap	661	66.5	4.8	1059	2	US-10-209-059-42	Sequence 42, Appli
589	67	4.8	506	2	US-09-134-000C-6170	Sequence 6170, Ap	662	66.5	4.8	1148	2	US-09-900-237-4	Sequence 4, Appli
590	67	4.8	519	2	US-09-719-919A-17	Sequence 17, Appli	663	66.5	4.8	1167	2	US-09-008-097-6	Sequence 6, Appli
591	67	4.8	541	2	US-09-716-129-54	Sequence 54, Appli	664	66.5	4.8	1167	2	US-09-472-667-6	Sequence 6, Appli
592	67	4.8	545	2	US-09-902-540-10576	Sequence 10576, A	665	66.5	4.8	1548	2	US-10-418-036-14	Sequence 14, Appli
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595	67	4.8	590	2	US-09-902-540-14944	Sequence 14944, A	668	66.5	4.8	1704	2	US-08-762-500-75	Sequence 75, Appli
596	67	4.8	601	2	US-09-134-000C-5783	Sequence 5783, Ap	669	66.5	4.8	1704	2	US-09-032-438C-120	Sequence 120, App
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607	67	4.8	1457	2	US-08-991-953A-3	Sequence 3, Appli	680	66	4.7	357	2	US-09-303-518D-850	Sequence 850, App
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696	66	4.7	511	1	US-08-278-635B-8	Sequence 8, Appli	769	65.5	4.7	697	2	US-09-603-208A-226	Sequence 226, App
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703	66	4.7	639	2	US-09-134-001C-5661	Sequence 5661, Ap	776	65.5	4.7	1036	2	US-09-398-239-5	Sequence 5, Appli
704	66	4.7	687	2	US-08-834-467-2	Sequence 2, Appli	777	65.5	4.7	1065	2	US-09-560-876A-5	Sequence 5, Appli
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706	66	4.7	687	2	US-09-248-796A-14715	Sequence 14715, A	779	65	4.7	144	2	US-09-134-001C-3102	Sequence 3102, Ap
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711	66	4.7	1724	2	US-09-564-899-43	Sequence 43, Appl	784	65	4.7	168	2	US-09-619-380-17	Sequence 17, Appl
712	66	4.7	4377	2	US-09-949-016-6978	Sequence 6978, Ap	785	65	4.7	168	2	US-09-527-376-12	Sequence 12, Appl
713	65.5	4.7	157	2	US-09-461-325-155	Sequence 155, App	786	65	4.7	168	2	US-09-527-376-12	Sequence 12, Appl
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716	65.5	4.7	160	2	US-09-270-767-49320	Sequence 49320, A	789	65	4.7	202	2	US-09-107-433-3144	Sequence 3144, Ap
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726	65.5	4.7	323	2	US-09-134-001C-4635	Sequence 4635, Ap	799	65	4.7	346	2	US-09-710-279-504	Sequence 504, App
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735	65.5	4.7	355	2	US-09-088-337B-32	Sequence 32, Appl	808	65	4.7	393	2	US-09-134-000C-4238	Sequence 4238, Ap
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737	65.5	4.7	355	2	US-09-170-496D-232	Sequence 232, App	810	65	4.7	405	2	US-09-543-681A-4311	Sequence 4311, Ap
738	65.5	4.7	355	2	US-09-917-254-68	Sequence 68, Appl	811	65	4.7	406	2	US-09-134-001C-4084	Sequence 4084, Ap
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755	65.5	4.7	428	2	US-09-443-745-31	Sequence 31, Appl	828	65	4.7	518	2	US-09-434-427-2	Sequence 2, Appli
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757	65.5	4.7	444	1	US-07-937-609-14	Sequence 14, Appl	830	65	4.7	518	2		

831	65	4.7	518	2	US-09-548-367D-2	Sequence 2, Appli	904	64.5	4.6	413	2	US-09-438-185A-838	Sequence 838, App
832	65	4.7	518	2	US-09-551-853D-2	Sequence 2, Appli	905	64.5	4.6	416	2	US-09-540-236-283	Sequence 2393, Ap
833	65	4.7	518	2	US-09-215-450-19	Sequence 19, Appl	906	64.5	4.6	431	2	US-09-900-237-28	Sequence 28, Appl
834	65	4.7	518	2	US-09-416-901B-2	Sequence 2, Appli	907	64.5	4.6	436	2	US-09-949-016-11448	Sequence 11448, A
835	65	4.7	518	2	US-09-548-376D-2	Sequence 2, Appli	908	64.5	4.6	439	2	US-09-710-279-2408	Sequence 2408, Ap
836	65	4.7	518	2	US-08-886-143-2	Sequence 2, Appli	909	64.5	4.6	439	2	US-09-134-001C-4856	Sequence 4856, Ap
837	65	4.7	518	2	US-09-794-927A-2	Sequence 2, Appli	910	64.5	4.6	462	2	US-09-902-540-10036	Sequence 10036, A
838	65	4.7	518	2	US-09-548-373D-2	Sequence 2, Appli	911	64.5	4.6	470	1	US-08-724-394A-10	Sequence 10, Appl
839	65	4.7	518	2	US-09-795-847B-2	Sequence 2, Appli	912	64.5	4.6	493	2	US-09-489-039A-13709	Sequence 13709, A
840	65	4.7	518	2	US-09-869-414-2	Sequence 2, Appli	913	64.5	4.6	517	2	US-09-815-923-16	Sequence 16, Appl
841	65	4.7	518	2	US-09-548-366B-2	Sequence 2, Appli	914	64.5	4.6	534	2	US-09-252-991A-31719	Sequence 31719, A
842	65	4.7	518	2	US-09-548-368B-2	Sequence 2, Appli	915	64.5	4.6	539	2	US-09-518-959-8	Sequence 8, Appli
843	65	4.7	518	2	US-09-794-925A-2	Sequence 2, Appli	916	64.5	4.6	539	2	US-09-518-959-9	Sequence 9, Appli
844	65	4.7	518	2	US-09-806-194A-2	Sequence 2, Appli	917	64.5	4.6	549	2	US-09-115-150-4	Sequence 4, Appli
845	65	4.7	518	2	US-09-668-314C-2	Sequence 2, Appli	918	64.5	4.6	549	2	US-09-489-039A-82337	Sequence 8237, Ap
846	65	4.7	518	2	US-09-668-314C-66	Sequence 66, Appl	919	64.5	4.6	550	2	US-09-721-870-18	Sequence 18, Appl
847	65	4.7	518	2	US-09-548-365-2	Sequence 2, Appli	920	64.5	4.6	555	2	US-09-543-681A-4582	Sequence 4582, Ap
848	65	4.7	518	2	US-09-794-743-2	Sequence 2, Appli	921	64.5	4.6	561	2	US-09-134-000C-4759	Sequence 4759, Ap
849	65	4.7	518	2	US-09-599-833A-196	Sequence 196, App	922	64.5	4.6	604	2	US-09-820-809-13	Sequence 13, Appl
850	65	4.7	518	2	US-10-020-445A-196	Sequence 196, App	923	64.5	4.6	613	2	US-09-328-352-7962	Sequence 7962, Ap
851	65	4.7	535	2	US-09-489-039A-13906	Sequence 13906, A	924	64.5	4.6	672	1	US-07-841-651-2	Sequence 2, Appli
852	65	4.7	541	1	US-08-967-101-166	Sequence 166, App	925	64.5	4.6	672	1	US-07-841-651-3	Sequence 3, Appli
853	65	4.7	541	1	US-08-592-541-166	Sequence 166, App	926	64.5	4.6	674	2	US-09-540-236-3546	Sequence 3546, Ap
854	65	4.7	541	2	US-08-888-077A-21	Sequence 21, Appl	927	64.5	4.6	677	2	US-09-543-681A-6388	Sequence 6388, Ap
855	65	4.7	541	2	US-09-124-698-166	Sequence 166, App	928	64.5	4.6	723	2	US-09-248-796A-15245	Sequence 15245, A
856	65	4.7	541	2	US-09-127-480-166	Sequence 166, App	929	64.5	4.6	741	2	US-09-605-703B-1584	Sequence 1584, Ap
857	65	4.7	541	2	US-09-124-523-166	Sequence 166, App	930	64.5	4.6	742	2	US-09-902-540-11489	Sequence 11489, A
858	65	4.7	541	2	US-09-636-796A-166	Sequence 166, App	931	64.5	4.6	870	2	US-09-949-016-11434	Sequence 11434, A
859	65	4.7	541	2	US-09-949-016-11075	Sequence 11075, A	932	64.5	4.6	878	2	US-09-949-016-11109	Sequence 11109, A
860	65	4.7	545	2	US-09-198-452A-519	Sequence 519, App	933	64.5	4.6	908	1	US-07-903-456-2	Sequence 2, Appli
861	65	4.7	545	2	US-09-438-185A-483	Sequence 483, App	934	64.5	4.6	908	2	US-08-666-221B-6	Sequence 6, Appli
862	65	4.7	562	2	US-09-328-352-4694	Sequence 4694, App	935	64.5	4.6	908	2	US-08-249-241-2	Sequence 2, Appli
863	65	4.7	574	2	US-09-107-433-3877	Sequence 3877, Ap	936	64.5	4.6	908	2	US-09-949-016-7025	Sequence 7025, Ap
864	65	4.7	599	1	US-08-222-619-2	Sequence 2, Appli	937	64.5	4.6	912	4	PCT-US91-09422-19	Sequence 19, Appl
865	65	4.7	599	2	US-08-221-767-24	Sequence 24, Appl	938	64.5	4.6	1071	1	US-08-975-527-1	Sequence 1, Appli
866	65	4.7	599	4	PCT-US95-04075-2	Sequence 2, Appli	939	64.5	4.6	1122	2	US-09-489-039A-8554	Sequence 8554, Ap
867	65	4.7	633	2	US-09-248-796A-20407	Sequence 20407, A	940	64	4.6	125	2	US-09-270-767-36480	Sequence 36480, A
868	65	4.7	682	2	US-09-744-926-2	Sequence 2, Appli	941	64	4.6	125	2	US-09-270-767-51697	Sequence 51697, A
869	65	4.7	738	2	US-09-107-532A-5096	Sequence 5096, Ap	942	64	4.6	135	2	US-09-270-767-32080	Sequence 32080, A
870	65	4.7	768	2	US-09-120-653D-5	Sequence 5, Appli	943	64	4.6	171	2	US-09-902-540-10737	Sequence 10737, A
871	65	4.7	1095	2	US-09-636-215-780	Sequence 780, App	944	64	4.6	179	2	US-09-902-540-11797	Sequence 11797, A
872	65	4.7	1095	2	US-09-685-166A-780	Sequence 780, App	945	64	4.6	205	2	US-09-540-236-2955	Sequence 2955, Ap
873	65	4.7	1095	2	US-09-679-426-780	Sequence 780, App	946	64	4.6	238	2	US-09-247-155-89	Sequence 89, Appl
874	65	4.7	1095	2	US-09-759-143-780	Sequence 780, App	947	64	4.6	238	2	US-09-903-190-89	Sequence 89, Appl
875	65	4.7	1095	2	US-09-651-236-780	Sequence 780, App	948	64	4.6	250	2	US-09-543-681A-4487	Sequence 4487, Ap
876	65	4.7	1095	2	US-09-657-279-780	Sequence 780, App	949	64	4.6	258	2	US-09-328-352-4425	Sequence 4425, Ap
877	65	4.7	1095	2	US-10-012-896-780	Sequence 780, App	950	64	4.6	264	2	US-09-107-532A-5290	Sequence 5290, Ap
878	65	4.7	1104	2	US-09-793-998-11	Sequence 11, Appl	951	64	4.6	296	2	US-09-724-623-103	Sequence 103, App
879	65	4.7	3174	1	US-08-477-451-3	Sequence 3, Appli	952	64	4.6	315	2	US-09-134-001C-3561	Sequence 3561, Ap
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881	64.5	4.6	173	2	US-09-270-767-3313	Sequence 3313, A	954	64	4.6	344	2	US-09-110-116-4	Sequence 4, Appli
882	64.5	4.6	173	2	US-09-270-767-48530	Sequence 48530, A	955	64	4.6	355	2	US-09-170-496D-164	Sequence 164, App
883	64.5	4.6	238	2	US-09-134-001C-3136	Sequence 3136, Ap	956	64	4.6	357	2	US-09-303-518D-848	Sequence 848, App
884	64.5	4.6	240	2	US-09-543-681A-5483	Sequence 5483, Ap	957	64	4.6	369	2	US-08-462-509B-4	Sequence 4, Appli
885	64.5	4.6	256	2	US-10-104-047-2400	Sequence 2400, Ap	958	64	4.6	369	4	PCT-US95-05616-6	Sequence 4, Appli
886	64.5	4.6	259	2	US-09-489-039A-11949	Sequence 11949, A	959	64	4.6	371	2	US-09-328-352-7132	Sequence 7132, Ap
887	64.5	4.6	260	2	US-08-983-075D-9	Sequence 9, Appli	960	64	4.6	372	2	US-08-462-509B-6	Sequence 6, Appli
888	64.5	4.6	263	2	US-09-949-016-10927	Sequence 10927, A	961	64	4.6	374	2	US-09-045-583-48	Sequence 48, Appl
889	64.5	4.6	276	2	US-09-583-110-5031	Sequence 5031, Ap	962	64	4.6	374	2	US-09-534-185-48	Sequence 48, Appl
890	64.5	4.6	284	2	US-09-107-433-3147	Sequence 3147, App	963	64	4.6	374	2	US-09-514-098-58	Sequence 58, Appl
891	64.5	4.6	323	2	US-09-489-039A-7408	Sequence 7408, Ap	964	64	4.6	377	4	PCT-US95-05616-6	Sequence 6, Appli
892	64.5	4.6	338	2	US-09-270-767-34974	Sequence 34974, A	965	64	4.6	380	2	US-09-097-889-25	Sequence 25, Appl
893	64.5	4.6	338	2	US-09-270-767-50191	Sequence 50191, A	966	64	4.6	380	2	US-09-097-889-25	Sequence 25, Appl
894	64.5	4.6	344	2	US-08-111-731A-172	Sequence 172, App	967	64	4.6	386	2	US-09-813-131A-2	Sequence 2, Appli
895	64.5	4.6	381	2	US-09-248-796A-20097	Sequence 20097, A	968	64	4.6	386	2	US-09-248-796A-16627	Sequence 16627, A
896	64.5	4.6	398	2	US-09-348-930A-9	Sequence 9, Appli	969	64	4.6	386	2	US-10-212-877-2	Sequence 2, Appli
897	64.5	4.6	398	2	US-09-578-063-75	Sequence 75, App	970	64	4.6	389	1	US-08-846-705-2	Sequence 23, Appl
898	64.5	4.6	399	2	US-09-328-352-7394	Sequence 7394, Ap	971	64	4.6	389	2	US-09-211-823C-23	Sequence 23, Appl
899	64.5	4.6	404	2	US-09-489-039A-8947	Sequence 8947, Ap	972	64	4.6	394	2	US-09-710-279-3292	Sequence 3292, Ap
900	64.5	4.6	411	2	US-08-887-534A-80	Sequence 80, Appl	973	64	4.6	398	2	US-09-489-039A-13159	Sequence 13159, A
901	64.5	4.6	411	2	US-09-527-431-80	Sequence 80, Appl	974	64	4.6	402	2	US-08-846-704-4	Sequence 4, Appli
902	64.5	4.6	411	2	US-09-446-861-80	Sequence 80, Appl	975	64	4.6	402	2	US-08-462-509B-2	Sequence 2, Appli
903	64.5	4.6	412	2	US-09-198-452A-901	Sequence 901, App	976	64	4.6	402	4	PCT-US95-05616-2	Sequence 2, Appli

977	64	4.6	415	2	US-09-134-000C-4092	Sequence 4092, Ap	1050	63.5	4.6	391	2	US-09-489-039A-9791	Sequence 9791, Ap
978	64	4.6	425	2	US-08-846-704-2	Sequence 2, Appli	1051	63.5	4.6	404	1	US-08-428-243-7	Sequence 7, Appli
979	64	4.6	425	2	US-09-479-128-2	Sequence 22, Appli	1052	63.5	4.6	404	4	PCT-US93-10301-7	Sequence 7, Appli
980	64	4.6	425	2	US-09-211-823C-22	Sequence 22, Appli	1053	63.5	4.6	405	2	US-09-248-796A-17965	Sequence 17965, Ap
981	64	4.6	425	2	US-09-826-509-549	Sequence 549, App	1054	63.5	4.6	414	2	US-09-489-039A-10869	Sequence 10869, A
982	64	4.6	428	2	US-09-345-236B-62	Sequence 62, Appli	1055	63.5	4.6	430	2	US-09-583-110-4230	Sequence 4230, Ap
983	64	4.6	430	1	US-08-601-435-2	Sequence 2, Appli	1056	63.5	4.6	430	2	US-09-248-796A-14556	Sequence 14556, A
984	64	4.6	430	1	US-08-931-047-2	Sequence 2, Appli	1057	63.5	4.6	437	2	US-09-107-433-3678	Sequence 3678, Ap
985	64	4.6	430	1	US-08-783-202-2	Sequence 2, Appli	1058	63.5	4.6	449	2	US-09-949-016-8594	Sequence 8594, Ap
986	64	4.6	430	2	US-09-443-041A-31	Sequence 31, Appli	1059	63.5	4.6	457	2	US-09-721-870-26	Sequence 26, Appli
987	64	4.6	441	2	US-09-583-110-4400	Sequence 4400, Ap	1060	63.5	4.6	458	2	US-09-328-352-5083	Sequence 5083, Ap
988	64	4.6	445	2	US-09-107-433-5039	Sequence 5039, Ap	1061	63.5	4.6	470	2	US-09-543-681A-4625	Sequence 4625, Ap
989	64	4.6	450	2	US-09-134-001C-4858	Sequence 4858, Ap	1062	63.5	4.6	473	1	US-08-439-131A-4	Sequence 4, Appli
990	64	4.6	450	2	US-09-252-991A-28134	Sequence 28134, A	1063	63.5	4.6	473	1	US-08-440-674-3	Sequence 3, Appli
991	64	4.6	452	2	US-09-489-039A-12558	Sequence 12558, A	1064	63.5	4.6	473	2	US-08-879-337-7	Sequence 7, Appli
992	64	4.6	458	3	US-09-041-075A-11	Sequence 11, Appli	1065	63.5	4.6	473	2	US-09-303-518D-378	Sequence 378, App
993	64	4.6	476	2	US-09-134-001C-3778	Sequence 3778, Ap	1066	63.5	4.6	476	2	US-09-489-039A-10203	Sequence 10203, A
994	64	4.6	495	2	US-09-359-167-2	Sequence 2, Appli	1067	63.5	4.6	482	2	US-09-328-352-7784	Sequence 7784, Ap
995	64	4.6	495	2	US-09-915-181A-7	Sequence 7, Appli	1068	63.5	4.6	488	1	US-08-115-365-2	Sequence 2, Appli
996	64	4.6	501	2	US-09-328-352-6371	Sequence 6371, Ap	1069	63.5	4.6	488	1	US-08-586-897-2	Sequence 2, Appli
997	64	4.6	522	2	US-09-502-540-12496	Sequence 12496, A	1070	63.5	4.6	488	2	US-09-826-509-561	Sequence 561, App
998	64	4.6	533	1	US-08-294-872-2	Sequence 2, Appli	1071	63.5	4.6	521	2	US-08-956-322-4	Sequence 4, Appli
999	64	4.6	533	1	PCT-US95-09823-2	Sequence 2, Appli	1072	63.5	4.6	531	2	US-09-489-039A-9781	Sequence 9781, Ap
1000	64	4.6	536	2	US-09-359-167-8	Sequence 8, Appli	1073	63.5	4.6	534	2	US-09-710-279-920	Sequence 920, App
1001	64	4.6	543	2	US-09-605-703B-1198	Sequence 1198, Ap	1074	63.5	4.6	542	2	US-09-830-123-2	Sequence 2, Appli
1002	64	4.6	585	2	US-09-949-016-7705	Sequence 7705, Ap	1075	63.5	4.6	557	2	US-09-902-540-12884	Sequence 12884, A
1003	64	4.6	602	2	US-09-605-703B-1200	Sequence 1200, Ap	1076	63.5	4.6	571	2	US-09-248-796A-20375	Sequence 20375, A
1004	64	4.6	613	2	US-09-107-532A-6935	Sequence 6935, Ap	1077	63.5	4.6	600	2	US-09-902-540-14821	Sequence 14821, A
1005	64	4.6	615	2	US-09-107-532A-6507	Sequence 6507, Ap	1078	63.5	4.6	650	2	US-08-800-291B-4	Sequence 4, Appli
1006	64	4.6	671	2	US-09-328-352-7868	Sequence 7868, Ap	1079	63.5	4.6	652	2	US-09-110-116-1	Sequence 1, Appli
1007	64	4.6	696	2	US-09-107-532A-4163	Sequence 4163, Ap	1080	63.5	4.6	652	2	US-08-956-322-2	Sequence 2, Appli
1008	64	4.6	771	2	US-09-252-991A-23521	Sequence 23521, A	1081	63.5	4.6	658	2	US-09-492-709A-352	Sequence 352, App
1009	64	4.6	816	2	US-09-248-796A-20939	Sequence 20939, A	1082	63.5	4.6	658	2	US-09-538-052-1190	Sequence 1190, Ap
1010	64	4.6	823	2	US-09-949-016-6852	Sequence 6852, Ap	1083	63.5	4.6	685	2	US-09-720-317A-31	Sequence 31, Appli
1011	64	4.6	846	2	US-09-949-016-10381	Sequence 10381, A	1084	63.5	4.6	689	2	US-09-248-796A-15264	Sequence 15264, A
1012	64	4.6	902	2	US-10-043-418-4	Sequence 4, Appli	1085	63.5	4.6	716	2	US-09-303-518D-106	Sequence 106, App
1013	64	4.6	1042	2	US-09-512-250C-32	Sequence 32, Appli	1086	63.5	4.6	769	2	US-10-191-436A-8	Sequence 8, Appli
1014	64	4.6	1063	2	US-09-248-796A-44361	Sequence 44361, A	1087	63.5	4.6	790	2	US-09-543-681A-5459	Sequence 5459, Ap
1015	64	4.6	1094	2	US-09-712-363-287	Sequence 287, App	1088	63.5	4.6	799	2	US-10-104-047-2335	Sequence 2335, Ap
1016	64	4.6	1278	2	US-09-462-136-2	Sequence 2, Appli	1089	63.5	4.6	803	2	US-09-543-681A-6767	Sequence 6767, Ap
1017	64	4.6	1318	2	US-09-949-016-10152	Sequence 10152, A	1090	63.5	4.6	850	2	US-09-583-110-4394	Sequence 4394, Ap
1018	64	4.6	1551	2	US-09-437-568A-46	Sequence 46, Appli	1091	63.5	4.6	861	2	US-09-107-433-2860	Sequence 2860, Ap
1019	64	4.6	1551	2	US-10-418-036-12	Sequence 12, Appli	1092	63.5	4.6	923	2	US-09-397-885-1	Sequence 1, Appli
1020	63.5	4.6	175	2	US-08-858-207A-363	Sequence 363, App	1093	63.5	4.6	923	2	US-09-969-362-1	Sequence 1, Appli
1021	63.5	4.6	221	2	US-09-248-796A-16290	Sequence 16290, A	1094	63.5	4.6	977	2	US-10-104-047-2552	Sequence 2552, Ap
1022	63.5	4.6	232	2	US-09-902-540-12730	Sequence 12730, A	1095	63.5	4.6	1007	2	US-10-209-059-28	Sequence 28, Appli
1023	63.5	4.6	237	2	US-08-768-859A-21	Sequence 21, Appli	1096	63.5	4.6	1065	2	US-09-221-013A-10	Sequence 10, Appli
1024	63.5	4.6	237	2	US-08-767-820A-21	Sequence 21, Appli	1097	63.5	4.6	1098	1	US-08-726-214-10	Sequence 10, Appli
1025	63.5	4.6	237	2	US-08-622-046B-1	Sequence 1, Appli	1098	63.5	4.6	1895	1	US-08-619-554-4	Sequence 4, Appli
1026	63.5	4.6	237	2	US-09-100-264-12	Sequence 12, Appli	1099	63.5	4.6	1895	2	US-09-487-558B-136	Sequence 136, App
1027	63.5	4.6	237	2	US-08-843-076D-8	Sequence 8, Appli	1100	63.5	4.6	2522	2	US-09-251-645-13	Sequence 13, Appli
1028	63.5	4.6	244	2	US-08-622-046B-5	Sequence 5, Appli	1101	63	4.5	138	2	US-09-583-110-4890	Sequence 4890, Ap
1029	63.5	4.6	247	2	US-09-489-039A-8478	Sequence 8478, Ap	1102	63	4.5	143	2	US-09-107-433-4477	Sequence 4477, Ap
1030	63.5	4.6	250	2	US-09-134-001C-4399	Sequence 4399, Ap	1103	63	4.5	154	2	US-09-248-796A-20059	Sequence 20059, A
1031	63.5	4.6	250	2	US-09-949-016-10962	Sequence 10962, A	1104	63	4.5	175	2	US-09-543-681A-8328	Sequence 8328, Ap
1032	63.5	4.6	261	2	US-08-768-859A-19	Sequence 19, Appli	1105	63	4.5	214	2	US-09-107-532A-5408	Sequence 5408, Ap
1033	63.5	4.6	261	2	US-08-767-820A-13	Sequence 13, Appli	1106	63	4.5	219	1	US-08-186-529-4	Sequence 4, Appli
1034	63.5	4.6	269	2	US-08-622-046B-3	Sequence 3, Appli	1107	63	4.5	219	1	US-08-640-386A-4	Sequence 4, Appli
1035	63.5	4.6	279	2	US-09-252-991A-24283	Sequence 24283, A	1108	63	4.5	249	2	US-09-902-540-13089	Sequence 13089, A
1036	63.5	4.6	284	2	US-09-303-518D-246	Sequence 246, App	1109	63	4.5	250	2	US-09-107-532A-6270	Sequence 6270, Ap
1037	63.5	4.6	288	2	US-09-372-448A-2	Sequence 2, Appli	1110	63	4.5	253	1	US-08-265-087-4	Sequence 4, Appli
1038	63.5	4.6	289	2	US-09-372-424A-2	Sequence 2, Appli	1111	63	4.5	253	1	US-08-621-493-4	Sequence 4, Appli
1039	63.5	4.6	309	2	US-09-902-540-11246	Sequence 11246, A	1112	63	4.5	253	1	US-08-684-688-4	Sequence 4, Appli
1040	63.5	4.6	311	2	US-09-489-039A-13013	Sequence 13013, A	1113	63	4.5	253	1	US-08-965-687-4	Sequence 4, Appli
1041	63.5	4.6	328	2	US-09-489-039A-10986	Sequence 10986, A	1114	63	4.5	253	2	US-09-260-173-4	Sequence 4, Appli
1042	63.5	4.6	332	2	US-09-252-991A-29029	Sequence 29029, A	1115	63	4.5	253	2	US-09-924-703-6	Sequence 6, Appli
1043	63.5	4.6	332	2	US-09-252-991A-11791	Sequence 11791, A	1116	63	4.5	259	2	US-09-328-352-6237	Sequence 6237, Ap
1044	63.5	4.6	345	2	US-09-248-796A-20780	Sequence 20780, A	1117	63	4.5	259	2	US-09-602-777A-292	Sequence 292, App
1045	63.5	4.6	356	2	US-08-567-882-7	Sequence 7, Appli	1118	63	4.5	273	2	US-09-949-016-8333	Sequence 8333, Ap
1046	63.5	4.6	359	2	US-09-248-796A-17633	Sequence 17633, A	1119	63	4.5	279	2	US-09-489-039A-13210	Sequence 13210, A
1047	63.5	4.6	378	2	US-09-540-236-3528	Sequence 3528, Ap	1120	63	4.5	284	2	US-09-270-767-33635	Sequence 33635, A
1048	63.5	4.6	379	1	US-08-227-108-18	Sequence 18, Appli	1121	63	4.5	284	2	US-09-270-767-48852	Sequence 48852, A
1049	63.5	4.6	379	1	US-09-073-674-18	Sequence 18, Appli	1122	63	4.5	287	2	US-09-134-000C-5944	Sequence 5944, Ap

1123	63	4.5	289	2	US-09-540-236-2019	Sequence 2019, Ap	1196	63	4.5	2368	1	US-08-198-446B-15	Sequence 15, Appl
1124	63	4.5	290	2	US-09-910-174B-8	Sequence 8, Appli	1197	63	4.5	2368	1	US-08-870-693-15	Sequence 15, Appl
1125	63	4.5	290	2	US-09-620-461-8	Sequence 8, Appli	1198	63	4.5	2910	1	US-08-466-033-183	Sequence 183, App
1126	63	4.5	290	2	US-09-451-291-1	Sequence 1, Appli	1199	63	4.5	2910	1	US-08-444-733-183	Sequence 183, App
1127	63	4.5	290	2	US-09-645-069-4	Sequence 4, Appli	1200	63	4.5	2910	1	US-08-464-134-183	Sequence 183, App
1128	63	4.5	290	2	US-09-915-789A-17	Sequence 17, Appl	1201	63	4.5	2910	1	US-08-461-361-183	Sequence 183, App
1129	63	4.5	290	2	US-09-644-934-4	Sequence 4, Appli	1202	63	4.5	2910	1	US-08-485-910-183	Sequence 183, App
1130	63	4.5	299	2	US-09-583-110-2991	Sequence 2991, Ap	1203	63	4.5	2910	4	PCT-US95-06266-157	Sequence 157, App
1131	63	4.5	345	2	US-09-362-123A-2	Sequence 2, Appli	1204	62.5	4.5	117	2	US-09-422-569-10	Sequence 10, Appli
1132	63	4.5	345	2	US-09-107-532A-4426	Sequence 4426, Ap	1205	62.5	4.5	117	2	US-09-823-153-2	Sequence 2, Appli
1133	63	4.5	345	2	US-09-991-181-2	Sequence 2, Appli	1206	62.5	4.5	131	2	US-09-902-540-12460	Sequence 12460, A
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1135	63	4.5	345	2	US-09-997-333-2	Sequence 2, Appli	1208	62.5	4.5	176	2	US-09-248-796A-15652	Sequence 15652, A
1136	63	4.5	345	2	US-09-992-598-2	Sequence 2, Appli	1209	62.5	4.5	202	2	US-09-134-001C-5617	Sequence 5617, Ap
1137	63	4.5	346	2	US-09-149-476-493	Sequence 493, App	1210	62.5	4.5	207	2	US-09-543-681A-7271	Sequence 7271, Ap
1138	63	4.5	350	2	US-09-902-540-14418	Sequence 14418, A	1211	62.5	4.5	232	2	US-09-107-532A-3905	Sequence 3905, Ap
1139	63	4.5	354	2	US-09-270-767-45287	Sequence 45287, A	1212	62.5	4.5	234	2	US-09-710-279-2580	Sequence 2580, Ap
1140	63	4.5	361	2	US-09-543-681A-5180	Sequence 5180, Ap	1213	62.5	4.5	237	1	US-08-096-946-10	Sequence 10, Appl
1141	63	4.5	365	1	US-08-833-610-7	Sequence 7, Appli	1214	62.5	4.5	237	2	US-08-768-859A-16	Sequence 16, Appl
1142	63	4.5	365	2	US-08-834-033A-17	Sequence 17, Appl	1215	62.5	4.5	237	2	US-08-767-820A-16	Sequence 16, Appl
1143	63	4.5	365	2	US-09-377-452-7	Sequence 7, Appli	1216	62.5	4.5	237	2	US-08-622-046B-12	Sequence 12, Appl
1144	63	4.5	374	2	US-09-721-341-8	Sequence 8, Appli	1217	62.5	4.5	237	2	US-08-944-483-37	Sequence 37, Appl
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1147	63	4.5	387	2	US-09-688-069-17	Sequence 17, Appl	1220	62.5	4.5	237	4	PCT-US94-07329-10	Sequence 10, Appl
1148	63	4.5	391	2	US-09-710-279-1236	Sequence 1236, Ap	1221	62.5	4.5	238	4	PCT-US95-06157-16	Sequence 16, Appl
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1150	63	4.5	401	2	US-09-489-039A-9416	Sequence 9416, Ap	1223	62.5	4.5	238	4	US-08-767-820A-8	Sequence 8, Appli
1151	63	4.5	409	2	US-09-605-703B-2146	Sequence 2146, Ap	1224	62.5	4.5	238	4	PCT-US95-06157-8	Sequence 8, Appli
1152	63	4.5	422	2	US-09-134-001C-4048	Sequence 4048, Ap	1225	62.5	4.5	244	2	US-08-768-859A-10	Sequence 10, Appl
1153	63	4.5	424	2	US-09-543-681A-4762	Sequence 4762, Ap	1226	62.5	4.5	244	2	US-08-767-820A-16	Sequence 16, Appl
1154	63	4.5	425	2	US-09-543-681A-6042	Sequence 6042, Ap	1227	62.5	4.5	244	2	US-08-622-046B-16	Sequence 16, Appl
1155	63	4.5	430	2	US-09-443-041A-18	Sequence 18, Appl	1228	62.5	4.5	244	2	US-09-100-264-5	Sequence 5, Appli
1156	63	4.5	430	2	US-09-134-000C-4627	Sequence 4627, Ap	1229	62.5	4.5	244	2	US-08-843-076D-5	Sequence 5, Appli
1157	63	4.5	438	1	US-08-677-049-9	Sequence 9, Appli	1230	62.5	4.5	244	4	PCT-US95-06157-10	Sequence 10, Appl
1158	63	4.5	443	1	US-08-570-157-6	Sequence 6, Appli	1231	62.5	4.5	261	2	US-08-768-859A-6	Sequence 6, Appli
1159	63	4.5	443	2	US-09-076-510-6	Sequence 6, Appli	1232	62.5	4.5	261	2	US-08-767-820A-6	Sequence 6, Appli
1160	63	4.5	443	2	US-09-004-349-6	Sequence 6, Appli	1233	62.5	4.5	261	2	US-08-622-046B-14	Sequence 14, Appl
1161	63	4.5	454	2	US-09-830-230A-33	Sequence 33, Appl	1234	62.5	4.5	261	2	US-09-100-264-7	Sequence 7, Appli
1162	63	4.5	461	1	US-08-194-338-4	Sequence 4, Appli	1235	62.5	4.5	261	2	US-08-983-075D-7	Sequence 7, Appli
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1164	63	4.5	478	1	US-09-107-532A-6105	Sequence 6105, Ap	1237	62.5	4.5	261	4	PCT-US95-06157-6	Sequence 6, Appli
1165	63	4.5	478	2	US-09-949-016-6543	Sequence 6543, Ap	1238	62.5	4.5	276	2	US-09-134-001C-3456	Sequence 3456, Ap
1166	63	4.5	485	2	US-09-949-016-10465	Sequence 10465, A	1239	62.5	4.5	277	1	US-08-118-270-68	Sequence 68, Appl
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1170	63	4.5	554	2	US-09-540-236-2634	Sequence 2634, Ap	1243	62.5	4.5	291	2	US-09-393-634-64	Sequence 64, Appl
1171	63	4.5	580	2	US-09-657-252-2	Sequence 2, Appli	1244	62.5	4.5	291	2	US-09-949-016-6919	Sequence 6919, Ap
1172	63	4.5	597	1	US-09-328-352-4703	Sequence 4703, Ap	1245	62.5	4.5	292	2	US-09-949-016-8213	Sequence 8213, Ap
1173	63	4.5	611	1	US-08-677-049-2	Sequence 2, Appli	1246	62.5	4.5	292	2	US-09-543-681A-7918	Sequence 7918, Ap
1174	63	4.5	629	2	US-09-252-991A-17988	Sequence 17988, A	1247	62.5	4.5	299	2	US-09-769-787-82	Sequence 82, Appl
1175	63	4.5	659	2	US-09-252-991A-30353	Sequence 30353, A	1248	62.5	4.5	304	2	US-09-328-352-7098	Sequence 7098, Ap
1176	63	4.5	683	2	US-08-979-847B-208	Sequence 208, App	1249	62.5	4.5	323	2	US-09-540-236-2883	Sequence 2883, Ap
1177	63	4.5	683	2	US-08-979-847B-210	Sequence 210, App	1250	62.5	4.5	324	2	US-09-543-681A-5947	Sequence 5947, Ap
1178	63	4.5	831	2	US-10-055-364-39	Sequence 39, Appl	1251	62.5	4.5	325	2	US-09-107-532A-6542	Sequence 6542, Ap
1179	63	4.5	849	2	US-08-804-439A-17	Sequence 17, Appl	1252	62.5	4.5	332	2	US-09-252-991A-18980	Sequence 18980, A
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1182	63	4.5	970	2	US-09-795-927-7	Sequence 7, Appli	1255	62.5	4.5	351	2	US-09-949-016-11252	Sequence 11252, A
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1185	63	4.5	1079	2	US-09-489-039A-7502	Sequence 7502, Ap	1258	62.5	4.5	361	2	US-09-248-568-2	Sequence 2, Appli
1186	63	4.5	1168	2	US-09-313-942-24	Sequence 24, Appl	1259	62.5	4.5	361	2	US-09-364-425B-19	Sequence 19, Appl
1187	63	4.5	1168	2	US-10-282-162-24	Sequence 24, Appl	1260	62.5	4.5	361	2	US-09-364-425B-50	Sequence 50, Appl
1188	63	4.5	1221	2	US-09-919-891-2	Sequence 2, Appli	1261	62.5	4.5	371	2	US-09-636-215-708	Sequence 708, App
1189	63	4.5	2227	2	US-08-475-886-4	Sequence 4, Appli	1262	62.5	4.5	371	2	US-09-685-166A-708	Sequence 708, App
1190	63	4.5	2227	2	US-08-475-886-6	Sequence 6, Appli	1263	62.5	4.5	371	2	US-09-679-426-708	Sequence 708, App
1191	63	4.5	2227	2	US-08-397-232-4	Sequence 4, Appli	1264	62.5	4.5	371	2	US-09-759-143-708	Sequence 708, App
1192	63	4.5	2227	2	US-09-653-499-4	Sequence 4, Appli	1265	62.5	4.5	371	2	US-09-651-273-708	Sequence 708, App
1193	63	4.5	2227	2	US-09-653-499-6	Sequence 6, Appli	1266	62.5	4.5	371	2	US-09-657-279-708	Sequence 708, App
1194	63	4.5	2227	2	US-10-135-988-4	Sequence 4, Appli	1267	62.5	4.5	371	2	US-10-012-896-708	Sequence 708, App
1195	63	4.5	2227	2	US-10-135-988-6	Sequence 6, Appli	1268	62.5	4.5	373	2	US-09-107-532A-7048	Sequence 7048, Ap

1269	62.5	4.5	376	2	US-09-949-016-7545	Sequence 7545, Ap	1342	62.5	4.5	784	2	US-09-489-039A-14075	Sequence 14075, A
1270	62.5	4.5	380	2	US-09-149-045-2	Sequence 2, Appli	1343	62.5	4.5	822	2	US-09-248-796A-20139	Sequence 20139, A
1271	62.5	4.5	382	2	US-09-252-991A-32165	Sequence 32165, A	1344	62.5	4.5	877	1	US-08-486-270-12	Sequence 12, Appl
1272	62.5	4.5	392	2	US-09-489-039A-12520	Sequence 12520, A	1345	62.5	4.5	877	2	US-08-367-264-12	Sequence 12, Appl
1273	62.5	4.5	398	2	US-09-328-352-6136	Sequence 6136, Ap	1346	62.5	4.5	877	2	US-09-153-757-12	Sequence 12, Appl
1274	62.5	4.5	400	2	US-09-636-215-852	Sequence 852, Ap	1347	62.5	4.5	877	2	US-09-459-715-12	Sequence 12, Appl
1275	62.5	4.5	400	2	US-09-685-166A-852	Sequence 852, App	1348	62.5	4.5	883	1	US-08-106-433A-2	Sequence 2, Appli
1276	62.5	4.5	400	2	US-09-679-426-852	Sequence 852, App	1349	62.5	4.5	883	2	US-09-254-352B-16	Sequence 16, Appl
1277	62.5	4.5	400	2	US-09-759-143-852	Sequence 852, App	1350	62.5	4.5	883	2	US-09-254-344-2	Sequence 2, Appli
1278	62.5	4.5	400	2	US-09-651-276-852	Sequence 852, App	1351	62.5	4.5	889	1	US-08-118-101A-4	Sequence 4, Appli
1279	62.5	4.5	400	2	US-09-657-279-852	Sequence 852, App	1352	62.5	4.5	908	2	US-08-823-110-1	Sequence 1, Appli
1280	62.5	4.5	400	2	US-10-012-896-852	Sequence 852, App	1353	62.5	4.5	908	2	US-08-604-298-1	Sequence 1, Appli
1281	62.5	4.5	405	2	US-09-489-039A-9411	Sequence 9411, Ap	1354	62.5	4.5	919	2	US-08-377-503-2	Sequence 2, Appli
1282	62.5	4.5	409	2	US-09-328-352-5447	Sequence 5447, Ap	1355	62.5	4.5	919	2	US-08-178-019-2	Sequence 2, Appli
1283	62.5	4.5	415	2	US-09-603-208A-286	Sequence 286, App	1356	62.5	4.5	1032	2	US-09-949-016-10265	Sequence 10265, A
1284	62.5	4.5	415	2	US-09-605-703B-2080	Sequence 2080, Ap	1357	62.5	4.5	1032	2	US-09-332-522E-94	Sequence 94, Appl
1285	62.5	4.5	424	2	US-09-489-039A-9628	Sequence 9628, Ap	1358	62.5	4.5	1079	2	US-10-209-059-22	Sequence 22, Appl
1286	62.5	4.5	437	2	US-09-248-796A-16548	Sequence 16548, A	1359	62.5	4.5	1094	2	US-10-160-719A-26	Sequence 26, Appl
1287	62.5	4.5	437	2	US-09-830-433A-59	Sequence 59, Appl	1360	62.5	4.5	1094	2	US-10-160-719A-46	Sequence 46, Appl
1288	62.5	4.5	451	2	US-09-446-861-127	Sequence 127, App	1361	62.5	4.5	1094	2	US-10-209-059-18	Sequence 18, Appl
1289	62.5	4.5	451	2	US-09-925-637-22	Sequence 22, Appl	1362	62.5	4.5	1158	2	US-09-313-942-26	Sequence 26, Appl
1290	62.5	4.5	455	2	US-09-543-681A-5989	Sequence 5989, Ap	1363	62.5	4.5	1158	2	US-10-282-162-26	Sequence 26, Appl
1291	62.5	4.5	458	2	US-09-489-039A-13954	Sequence 13954, A	1364	62.5	4.5	1165	2	US-09-900-237-8	Sequence 8, Appli
1292	62.5	4.5	461	2	US-09-252-991A-28434	Sequence 28434, A	1365	62.5	4.5	1248	2	US-10-042-810-2	Sequence 2, Appli
1293	62.5	4.5	461	2	US-09-489-039A-9623	Sequence 9623, Ap	1366	62.5	4.5	1248	2	US-10-042-810-4	Sequence 4, Appli
1294	62.5	4.5	465	2	US-09-328-352-4343	Sequence 4343, Ap	1367	62.5	4.5	1338	2	US-09-631-603-2	Sequence 2, Appli
1295	62.5	4.5	467	2	US-08-706-344C-4	Sequence 4, Appli	1368	62.5	4.5	1495	2	US-10-037-417-111	Sequence 111, App
1296	62.5	4.5	469	2	US-09-328-352-5007	Sequence 5007, Ap	1369	62.5	4.5	1765	2	US-09-270-767-45587	Sequence 45587, A
1297	62.5	4.5	473	2	US-09-303-518D-380	Sequence 380, App	1370	62.5	4.5	1849	2	US-08-851-567B-49	Sequence 49, Appl
1298	62.5	4.5	480	2	US-09-107-532A-6160	Sequence 6160, Ap	1371	62.5	4.5	2516	2	US-08-851-567B-47	Sequence 47, Appl
1299	62.5	4.5	484	2	US-09-266-965-17	Sequence 17, Appl	1372	62.5	4.5	2516	2	US-09-817-514A-2	Sequence 2, Appli
1300	62.5	4.5	487	2	US-09-489-039A-12980	Sequence 12980, A	1373	62	4.5	103	2	US-09-543-681A-7951	Sequence 7951, Ap
1301	62.5	4.5	489	2	US-09-328-352-5330	Sequence 5330, Ap	1374	62	4.5	119	2	US-10-027-736A-25	Sequence 25, Appl
1302	62.5	4.5	503	2	US-09-248-796A-20120	Sequence 20120, A	1375	62	4.5	152	2	US-09-710-279-1488	Sequence 1488, Ap
1303	62.5	4.5	508	2	US-09-332-522E-4	Sequence 4, Appli	1376	62	4.5	152	2	US-09-710-279-3224	Sequence 2224, Ap
1304	62.5	4.5	513	1	US-08-390-162-6	Sequence 6, Appli	1377	62	4.5	159	2	US-09-134-001C-5575	Sequence 5575, Ap
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; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC53
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; CURRENT FILING DATE: 2001-11-16
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RESULT 2
US-09-990-444-23
; Sequence 23, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-09
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Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 HVGAVLTFGMSLYMFVQTILSYOMQPKIHGKQVFWIRLLIIVWCGVSALSMITCSSVL 180
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Db 181 HSGNFGTDLQKLNHPEDKGYVLHMITTAAPWSMSFSFSFFGFLTYIRDFQKISLRVEAN 240
QY 241 LHGLTYDTAPCPINNERTLLSRDI 266
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RESULT 3
US-09-997-333-23
; Sequence 23, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 1392; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.1e-144;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWFOGSLFSLPVSALVITSAAFIPSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAWL 60
DB 1 MMWFOGSLFSLPVSALVITSAAFIPSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAWL 60

QY 61 NIAAVLCIATIVYRYKQVHALSPEENVIIKLNKAGLVGLISCLGLSIVANFQKTTLFAA 120
DB 61 NIAAVLCIATIVYRYKQVHALSPEENVIIKLNKAGLVGLISCLGLSIVANFQKTTLFAA 120

QY 121 HVSGAVLTFGMSGLYMFVOTILSYOMQPKIHGKQVFWIRLLVIVWCGVSALMLTCSSVL 180
DB 121 HVSGAVLTFGMSGLYMFVOTILSYOMQPKIHGKQVFWIRLLVIVWCGVSALMLTCSSVL 180

QY 181 HSGNFGTDLQKLNWPKDGVVLHMITTAASMSFSFPGFPLTYIRDFQKISLRVEAN 240
DB 181 HSGNFGTDLQKLNWPKDGVVLHMITTAASMSFSFPGFPLTYIRDFQKISLRVEAN 240

QY 241 LHGLTYDTAPCPINNERTRLLSRDI 266
DB 241 LHGLTYDTAPCPINNERTRLLSRDI 266

RESULT 4
US-09-992-598-23
; Sequence 23, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
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; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 190
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-663-600A-190

Query Match          99.7%; Score 1388; DB 2; Length 267;
Best Local Similarity 99.6%; Pred. No. 2.9e-144;
Matches 265; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MWVFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWVFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVLCIATIIYVRKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120
Db 61 NIAAVLCIATIIYVRKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120
QY 121 HVSGAVLTFMGSLYMFVQTILSYOMQPKIHGQVFWIRLLLVWCGVSALSMLTCSSVL 180
Db 121 HVSGAVLTFMGSLYMFVQTILSYOMQPKIHGQVFWIRLLLVWCGVSALSMLTCSSVL 180
QY 181 HSGNFGTDLQKLNWPNEDKGYLVLMITTAAEWSMSFSFPGFFLYIRDFQKISLRVEAN 240
Db 181 HSGNFGTDLQKLNWPNEDKGYLVLMITTAAEWSMSFSFPGFFLYIRDFQKISLRVEAN 240
QY 241 LHGLTYDTAPCPINNERTLLSRDI 266
Db 241 LHGLTYDTAPCPINNERTLLSRDI 266
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RESULT 6
US-09-663-600A-96
; Sequence 96, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Bouqueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 96
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-663-600A-130
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-663-600A-96

Query Match          42.8%; Score 595.5; DB 2; Length 172;
Best Local Similarity 79.4%; Pred. No. 2.2e-57;
Matches 123; Conservative 7; Mismatches 22; Indels 3; Gaps 2;

QY 1 MWVFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWVFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVLCIATIIYVRKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120
Db 61 NIAAVLCIATIIYVRKQVHALSPENVIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120
QY 121 HVSGAVLTFMGSLYMFVQTILSYOMQPKIHGK 153
Db 121 TCKWSCAYLWYGL-IYYVSDHPFLPKCSPKSNKG 154

RESULT 7
US-09-724-864-38
; Sequence 38, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: By the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-38

Query Match          34.4%; Score 479.5; DB 2; Length 238;
Best Local Similarity 37.3%; Pred. No. 2e-44;
Matches 93; Conservative 56; Mismatches 79; Indels 21; Gaps 3;

QY 1 MWVFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MLCFLRGMAFVFLVLTWSSAAFIISYVAVLSGHVNPFLPYISDTGTPPESGIFGMI 60
QY 61 NIAAVLCIATIIYVRKQV-----HALSPENVIKLNKAGLVGLSCLGLSIVANFQ 113
Db 61 NFSAPLGAATMYTRYKIVEKQNETCYFTPTVFNLV-----SLALGLVCGICGMGIVANFQ 114
QY 114 KTLTFAAHVSGAVLTFMGSLYMFVQTILSYOMQPKIHGQVFWIRLLLVWCGVSALS 173
Db 115 ELAVPVVDGGALLAFVCGVVYVTLQSIISYKSCPOWNSLTCHVRMAISAVCAAVPM 174
QY 174 LTCSSVLHSGNFGTDLQKLNWPNEDKGYLVLMITTAAEWSMSFSFPGFFLYIRDFQKI 233
Db 175 IACASLISI-----TKLEWNPKEKDYIYHVVSALCEWTVAFGFIFVFLTFIQDFQSV 226
QY 234 SLRVEANLH 242
Db 227 TLRISTEIN 235

RESULT 8
US-09-663-600A-130
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; Sequence 130, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 130
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-4
US-09-663-600A-130

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Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWFOGSLFPLSALVINTSAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MMWFOGSLFPLSALVINTSAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVLC 67
Db 61 NIAAVLC 67

RESULT 9
US-09-663-600A-224
; Sequence 224, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273

; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 224
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-663-600A-224

Query Match 25.7%; Score 358; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 8.1e-32;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWFOGSLFPLSALVINTSAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MMWFOGSLFPLSALVINTSAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVLC 67
Db 61 NIAAVLC 67

RESULT 10
US-08-905-223-20
; Sequence 20, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..21
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVINTSA/AF
US-08-905-223-20

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MWFFQOGLSFLPSALVIWTS 21

RESULT 11
US-09-247-155-20
; Sequence 20, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 20
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; TYPE: PRT
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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTS/AF
US-09-247-155-20

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Best Local Similarity 100.0%; Pred. No. 3.8e-06;
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DB 1 MWFFQOGLSFLPSALVIWTS 21

RESULT 12
US-09-663-600A-20
; Sequence 20, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; EARLIER APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09

; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 20
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTS/AF
US-09-663-600A-20

Query Match 8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWFFQOGLSFLPSALVIWTS 21
DB 1 MWFFQOGLSFLPSALVIWTS 21

RESULT 13
US-09-621-976-2
; Sequence 2, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-621-976-2

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Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWFFQOGLSFLPSALVIWTS 21
DB 1 MWFFQOGLSFLPSALVIWTS 21

RESULT 14
US-09-513-999C-2
; Sequence 2, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C

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; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
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; SEQ ID NO 2
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
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; NAME/KEY: SIGNAL
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US-09-513-999C-2

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Query Match      8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 MMWFQOGLSFLPSALVIWTS 21

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RESULT 15
US-09-471-276-2
; Sequence 2, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 2
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
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; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTS/AF
US-09-471-276-2

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Query Match      8.5%; Score 118; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
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Db       1 MMWFQOGLSFLPSALVIWTS 21

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Job time : 60 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 7, 2006, 16:28:21 ; Search time 43 Seconds
(without alignments)

595.201 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392

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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 80:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	98.5	7.1	1120	2	A10561
6	97	7.0	604	2	E72523
7	96	6.9	495	2	S43882
8	94	6.8	495	1	S16447
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15	91.5	6.6	373	2	T24487
16	91.5	6.6	712	2	T02479
17	90.5	6.5	614	2	E86194
18	90	6.5	400	2	C82503
19	90	6.5	492	2	S59107
20	90	6.5	528	2	S19366
21	89.5	6.4	440	2	B64090
22	89.5	6.4	443	2	A61706
23	89.5	6.4	495	2	G71019
24	89.5	6.4	599	2	T24333
25	89	6.4	428	2	A10034
26	89	6.4	757	2	T42693
27	88.5	6.4	430	2	E75217
28	88.5	6.4	844	2	T23656
29	88	6.3	1165	2	A46180

hemolysin III (ypl)
GGDEF family prote
metabolite transpo
hypothetical prote
bicyclomycin resis
glutathione-regula
transporter homolo
glycerophosphoryl
hypothetical prote
hypothetical prote
bicyclomycin resis
F22L4.12 protein -
spermidine/putresc
probable ABC sugar
NADH2 dehydrogenas
phosphate transpor
polysaccharide bios
adenylate cyclase
hypothetical prote
amino acid permeas
lipopolysaccharide
hypothetical prote
NADH2 dehydrogenas
hypothetical prote
iron-compound ABC
hypothetical prote
probable permease
hypothetical prote
probable polyamine
hypothetical prote
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hypothetical prote
putrescine-ornithi
probable amino aci
NADH2 dehydrogenas
ethanolaminephosph
probable aromatic
proline/betaine tr
NADH2 dehydrogenas
probable amino aci
hypothetical prote
probable ABC trans
purine permease [i
citrate transport
proline/betaine tr
cytochrome-c oxida
probable amino-aci
hypothetical prote
hypothetical prote
probable potassium
conserved hypothet
hypothetical prote
sugar ABC transpor
BAC18.12 protein -
F3H9.12 protein -
probable MFS trans
hypothetical prote
NADH2 dehydrogenas
NADH2 dehydrogenas
probable glycerol-
probable metal tra
probable transport
probable amino aci
hypothetical prote
hypothetical prote
NADH2 dehydrogenas

103	80.5	5.8	359	2	F90055	conserved hypother	176	77.5	5.6	363	2	A72771	hypothetical prote
104	80.5	5.8	385	2	T07130	probable amino aci	177	77.5	5.6	461	2	H85755	probable amino aci
105	80.5	5.8	433	2	AC0043	anaerobic C4-dicar	178	77.5	5.6	464	2	C83605	probable transport
106	80.5	5.8	473	2	G69789	sugar transporter	179	77.5	5.6	479	2	A90863	probable amino aci
107	80.5	5.8	528	2	E81186	L-lactate permease	180	77.5	5.6	499	2	AGC882	hypothetical prote
108	80.5	5.8	590	1	ORBYPR	arginine transport	181	77.5	5.6	506	2	F64862	hypothetical prote
109	80.5	5.8	637	2	S78171	heme lyase yajR -	182	77.5	5.6	510	2	D96741	hypothetical prote
110	80.5	5.8	728	2	T13794	NADH2 dehydrogenas	183	77.5	5.6	510	2	E71695	hypothetical prote
111	80	5.7	266	2	G83178	conserved hypother	184	77.5	5.6	513	2	A82432	sodium/solute symp
112	80	5.7	291	2	A97387	hypothetical prote	185	77.5	5.6	526	2	T01853	probable hexose tr
113	80	5.7	291	2	AB2605	hypothetical prote	186	77.5	5.6	532	1	S49345	cytochrome-c oxida
114	80	5.7	429	1	C41903	arsenical pump mem	187	77.5	5.6	535	2	S76103	hypothetical prote
115	80	5.7	702	2	T12141	NADH2 dehydrogenas	188	77.5	5.6	649	2	A69478	NADH2 dehydrogenas
116	80	5.7	902	2	C83964	cation-transportin	189	77.5	5.6	717	2	T46172	phenylalanine ammo
117	80	5.7	1123	2	T48586	hypothetical prote	190	77.5	5.6	1118	2	B83018	conserved hypother
118	79.5	5.7	323	2	T32279	hypothetical prote	191	77	5.5	282	2	AD1231	B. subtilis YxkD p
119	79.5	5.7	405	2	T42992	cyclin D - Caenorh	192	77	5.5	332	2	D95973	probable sugar upt
120	79.5	5.7	445	2	S77010	nickel resistance	193	77	5.5	417	2	F90270	amino acid permeas
121	79.5	5.7	499	2	F75059	NADH-dehydrogenase	194	77	5.5	438	2	G64962	shikimate transport
122	79.5	5.7	539	1	S49495	cytochrome-c oxida	195	77	5.5	438	2	B89855	amino acid permeas
123	79.5	5.7	542	2	AG3605	potassium efflux s	196	77	5.5	471	2	H90502	phosphate transport
124	79.5	5.7	570	2	A97546	cytochrome-c oxida	197	77	5.5	519	2	JQ0124	membrane protein S
125	79.5	5.7	598	2	E97546	cytochrome c oxida	198	77	5.5	551	1	A55582	cytochrome-c oxida
126	79.5	5.7	741	2	T13051	NADH2 dehydrogenas	199	77	5.5	579	2	AB2177	hypothetical prote
127	79.5	5.7	831	2	B40204	Na+/H+-exchanging	200	77	5.5	662	2	H84984	bo-type ubiquinol
128	79	5.7	172	2	S55015	NADH2 dehydrogenas	201	77	5.5	710	2	T20635	hypothetical prote
129	79	5.7	183	2	A64009	hypothetical prote	202	77	5.5	739	2	T13038	NADH2 dehydrogenas
130	79	5.7	281	2	T26244	hypothetical prote	203	77	5.5	749	2	E71275	hypothetical integ
131	79	5.7	293	2	B83783	hypothetical prote	204	77	5.5	915	2	H96709	hypothetical prote
132	79	5.7	293	2	H72064	ABC transporter, p	205	77	5.5	936	2	T26521	hypothetical prote
133	79	5.7	303	2	C86558	metal transport pr	206	76.5	5.5	152	2	C72681	hypothetical prote
134	79	5.7	307	2	C81862	conserved hypother	207	76.5	5.5	269	2	H69768	conserved hypother
135	79	5.7	377	2	T49063	nodulin-like prote	208	76.5	5.5	284	2	G64052	probable formate t
136	79	5.7	390	2	H72265	hypothetical prote	209	76.5	5.5	289	2	T02095	transmembrane prot
137	79	5.7	395	2	D69312	molybdopterin oxid	210	76.5	5.5	300	2	S40858	hypothetical 32.9K
138	79	5.7	410	2	E84998	hypothetical prote	211	76.5	5.5	300	2	H91233	probable transport
139	79	5.7	438	2	B90976	shikimate transport	212	76.5	5.5	300	2	H86080	probable transport
140	79	5.7	444	2	G82392	conserved hypother	213	76.5	5.5	301	2	B82235	conserved hypother
141	79	5.7	453	2	AF1198	conserved hypother	214	76.5	5.5	301	2	T27585	hypothetical prote
142	79	5.7	472	2	T31717	hypothetical prote	215	76.5	5.5	305	2	D83699	hypothetical prote
143	79	5.7	489	2	B97289	lysine-specific pe	216	76.5	5.5	334	2	A75142	oligopeptide trans
144	79	5.7	685	2	T12139	NADH2 dehydrogenas	217	76.5	5.5	370	2	AB3334	daunorubicin resis
145	79	5.7	819	2	G69801	hypothetical prote	218	76.5	5.5	377	2	C89456	protein F55A4.8 fi
146	79	5.7	2198	2	T20371	hypothetical prote	219	76.5	5.5	382	2	B82177	Na+/H+ antiporter
147	78.5	5.6	169	2	H84191	hypothetical prote	220	76.5	5.5	395	2	AD0678	probable membrane
148	78.5	5.6	241	2	S00836	mcbE protein - Esc	221	76.5	5.5	431	2	H84069	hypothetical prote
149	78.5	5.6	366	2	C64449	cationic amino aci	222	76.5	5.5	474	2	F64119	NAD(P) transhydrog
150	78.5	5.6	405	2	T26678	hypothetical prote	223	76.5	5.5	475	2	E59643	histidine permease
151	78.5	5.6	412	2	G89773	hypothetical prote	224	76.5	5.5	495	2	AD0402	glycerol kinase [E
152	78.5	5.6	493	2	F75113	NADH dehydrogenase	225	76.5	5.5	548	2	B72542	probable cytochrom
153	78.5	5.6	579	2	A70954	hypothetical prote	226	76.5	5.5	725	2	S64124	probable membrane
154	78.5	5.6	622	2	E69609	cytochrome-c oxida	227	76.5	5.5	746	2	T13698	NADH2 dehydrogenas
155	78.5	5.6	624	2	T48587	peptide transporte	228	76.5	5.5	855	2	T47534	hypothetical prote
156	78.5	5.6	732	2	T13814	NADH2 dehydrogenas	229	76.5	5.5	1187	2	T20544	hypothetical prote
157	78.5	5.6	744	2	T13485	NADH2 dehydrogenas	230	76.5	5.5	1342	2	E85614	cell division prot
158	78.5	5.6	1325	2	T01037	hypothetical prote	231	76.5	5.5	1342	2	G80750	cell division prot
159	78	5.6	158	2	T26519	hypothetical prote	232	76	5.5	261	2	A64066	probable membrane
160	78	5.6	307	2	D81082	conserved hypother	233	76	5.5	275	2	C37028	probable metal-bin
161	78	5.6	335	2	E81736	phospho-N-acetylmu	234	76	5.5	281	2	AB1585	B. subtilis YxkD p
162	78	5.6	382	2	E97742	hypothetical prote	235	76	5.5	282	2	D97767	hypothetical prote
163	78	5.6	388	2	G75375	hypothetical prote	236	76	5.5	336	2	T23902	hypothetical prote
164	78	5.6	396	2	AF0785	bicyclomycin resis	237	76	5.5	365	2	F82210	amino acid ABC tra
165	78	5.6	414	2	S53075	probable membrane	238	76	5.5	415	2	G83568	probable permease
166	78	5.6	422	2	H64489	hypothetical prote	239	76	5.5	447	2	C84306	hypothetical prote
167	78	5.6	462	2	T06299	acetate-CoA ligase	240	76	5.5	452	2	S46037	prephenate dehydro
168	78	5.6	688	2	T48661	potassium transport	241	76	5.5	480	2	G83414	cytochrome-c oxida
169	78	5.6	701	2	T15238	hypothetical prote	242	76	5.5	502	2	JN0113	nicotinic acetylch
170	77.5	5.6	212	2	H95936	hypothetical prote	243	76	5.5	558	2	S08270	cytochrome-c oxida
171	77.5	5.6	283	2	E95887	probable ABC trans	244	76	5.5	578	2	T13664	NADH2 dehydrogenas
172	77.5	5.6	292	2	AD1182	sugar ABC transport	245	76	5.5	617	2	T20409	hypothetical prote
173	77.5	5.6	293	2	AH0143	probable membrane	246	76	5.5	659	2	E85889	probable oxidoredu
174	77.5	5.6	296	2	C95326	Atta22-like ABC tra	247	76	5.5	659	2	B91045	probable oxidoredu
175	77.5	5.6	335	2	A72289	oligopeptide ABC t	248	76	5.5	669	1	DNMU5	NADH2 dehydrogenas

249	249	76	5.5	956	2	A89153	protein C24B5.3 [i	322	74.5	5.4	411	2	T03836	phosphate/phospho
250	250	76	5.5	958	2	AC0204	probable integral	323	74.5	5.4	439	2	AB0389	branched-chain ami
251	251	76	5.5	966	2	H97717	hypothetical prote	324	74.5	5.4	447	2	T19112	hypothetical prote
252	252	76	5.5	971	2	H71719	hypothetical prote	325	74.5	5.4	469	1	BDEC	melibiose carrier
253	253	76	5.5	1052	2	T50127	hypothetical prote	326	74.5	5.4	469	2	C86107	melibiose permease
254	254	76	5.5	1074	2	T45094	probable arabinosy	327	74.5	5.4	469	2	F91266	melibiose permease
255	255	76	5.5	1166	2	A49201	adenylate cyclase	328	74.5	5.4	476	2	AG0502	probable amino-aci
256	256	75.5	5.4	210	2	T01623	hypothetical prote	329	74.5	5.4	544	2	T32895	hypothetical prote
257	257	75.5	5.4	237	2	A99737	hypothetical prote	330	74.5	5.4	560	2	T32727	hypothetical prote
258	258	75.5	5.4	237	2	B85587	hypothetical prote	331	74.5	5.4	726	2	T12215	NADH2 dehydrogenas
259	259	75.5	5.4	240	2	D71939	hypothetical prote	332	74.5	5.4	889	2	AD2215	two-component hybr
260	260	75.5	5.4	252	2	B47188	hypothetical prote	333	74.5	5.4	953	2	S19427	probable membrane
261	261	75.5	5.4	295	1	Q0SABT	MHC class II histo	334	74	5.3	277	2	E72030	conserved hypothet
262	262	75.5	5.4	296	2	B83049	hypothetical prote	335	74	5.3	281	2	A86594	CT560 hypothetical
263	263	75.5	5.4	297	2	AE0400	conserved hypothet	336	74	5.3	281	2	H90387	hypothetical prote
264	264	75.5	5.4	322	2	A12880	probable membrane	337	74	5.3	296	2	C69635	transcription repr
265	265	75.5	5.4	322	2	A97657	ABC transporter, m	338	74	5.3	303	2	T25501	hypothetical prote
266	266	75.5	5.4	338	2	C83785	ferrichrome ABC tr	339	74	5.3	322	1	A29928	membrane-associate
267	267	75.5	5.4	397	2	D69538	arsenite transport	340	74	5.3	370	2	H84351	hypothetical prote
268	268	75.5	5.4	432	2	A42476	hypothetical prote	341	74	5.3	380	2	S34964	hypothetical prote
269	269	75.5	5.4	432	2	AD0766	probable O-antigen	342	74	5.3	400	2	F86887	rhc protein - Shig
270	270	75.5	5.4	441	2	B71027	probable nfeD prot	343	74	5.3	401	2	E82951	hypothetical prote
271	271	75.5	5.4	454	2	E85826	probable amino aci	344	74	5.3	404	2	A36865	probable MFS trans
272	272	75.5	5.4	454	2	H90980	probable amino aci	345	74	5.3	407	2	G81010	ammonium transport
273	273	75.5	5.4	454	2	E64966	probable amino aci	346	74	5.3	425	2	H71554	conserved hypothet
274	274	75.5	5.4	454	2	AG0763	probable amino aci	347	74	5.3	431	2	T41614	hypothetical prote
275	275	75.5	5.4	459	2	S42238	tetracyclin resist	348	74	5.3	437	2	G82032	malate permease -
276	276	75.5	5.4	476	2	S23576	melibiose transpor	349	74	5.3	446	2	A42661	citrate carrier pr
277	277	75.5	5.4	492	2	AC0768	probable transmem	350	74	5.3	446	2	AD0509	citrate carrier pr
278	278	75.5	5.4	513	2	T39534	hypothetical prote	351	74	5.3	446	2	B42661	citrate carrier pr
279	279	75.5	5.4	532	2	D95287	conserved hypothet	352	74	5.3	459	2	T11084	NADH2 dehydrogenas
280	280	75.5	5.4	567	2	B81408	probable thiol-dis	353	74	5.3	473	2	AG0948	probable membrane
281	281	75.5	5.4	676	1	S54750	cytochrome c-type	354	74	5.3	508	2	A83839	hypothetical prote
282	282	75.5	5.4	735	2	F84726	probable Na+/H+ an	355	74	5.3	530	2	F85768	PTS system, maltos
283	283	75.5	5.4	740	2	T12223	NADH2 dehydrogenas	356	74	5.3	530	2	A99920	PTS system, maltos
284	284	75.5	5.4	832	2	A40205	Na+/H+-exchanging	357	74	5.3	532	2	H96840	hypothetical prote
285	285	75.5	5.4	914	2	I40529	penicillin-binding	358	74	5.3	542	2	F90457	hypothetical prote
286	286	75.5	5.4	932	2	T25941	hypothetical prote	359	74	5.3	592	2	T25837	hypothetical prote
287	287	75	5.4	262	2	B83827	hypothetical prote	360	74	5.3	612	2	C90419	glucan 1,4 alpha g
288	288	75	5.4	289	2	T12037	probable aquaporin	361	74	5.3	740	2	AH0600	probable membrane
289	289	75	5.4	291	2	T04139	transmembrane prot	362	74	5.3	817	2	T51787	hypothetical prote
290	290	75	5.4	298	2	S75972	hypothetical prote	363	74	5.3	908	2	S51293	hypothetical prote
291	291	75	5.4	322	2	B98193	sugar ABC transpor	364	74	5.3	947	2	H85088	hypothetical prote
292	292	75	5.4	322	2	AH3093	hypothetical prote	365	73.5	5.3	218	1	D69372	osmoprotection pro
293	293	75	5.4	395	2	S73531	CDP-diglyceride sy	366	73.5	5.3	240	2	A64652	hypothetical prote
294	294	75	5.4	398	2	B71193	hypothetical prote	367	73.5	5.3	299	2	B83323	hypothetical prote
295	295	75	5.4	429	1	B41902	arsenical pump mem	368	73.5	5.3	329	2	AD0442	probable branched-
296	296	75	5.4	432	2	H71092	hypothetical prote	369	73.5	5.3	337	2	T23942	hypothetical prote
297	297	75	5.4	451	2	E90171	inorganic phosphat	370	73.5	5.3	343	2	G86709	hypothetical prote
298	298	75	5.4	461	2	AF1179	hexose phosphate t	371	73.5	5.3	363	2	AF2457	hypothetical prote
299	299	75	5.4	494	2	A82294	probable carbon at	372	73.5	5.3	372	2	A98157	hypothetical prote
300	300	75	5.4	507	2	A11739	amino acid antipor	373	73.5	5.3	372	2	AH3130	ABC transporter, m
301	301	75	5.4	559	2	T33168	hypothetical prote	374	73.5	5.3	391	2	S30046	potassium channel
302	302	75	5.4	599	2	T48383	uracil transporter	375	73.5	5.3	409	2	T03718	suppressor 2 prote
303	303	75	5.4	625	2	D45335	cytochrome-c oxida	376	73.5	5.3	423	2	C81266	probable efflux pr
304	304	75	5.4	643	2	E69373	conserved hypothet	377	73.5	5.3	425	2	C65100	hypothetical 46.6
305	305	75	5.4	917	2	I49699	glycoprotein 130 -	378	73.5	5.3	426	2	D72049	phosphate permease
306	306	75	5.4	1056	2	G84865	hypothetical prote	379	73.5	5.3	443	2	F85972	probable transport
307	307	75	5.4	1294	2	S77690	probable membrane	380	73.5	5.3	443	2	G91127	probable transport
308	308	74.5	5.4	174	2	F90494	conserved hypothet	381	73.5	5.3	463	2	F90285	metabolite transpo
309	309	74.5	5.4	288	2	T09794	major intrinsic pr	382	73.5	5.3	476	2	AC1023	melibiose carrier
310	310	74.5	5.4	293	2	A96209	motC protein (impo	383	73.5	5.3	477	2	F82200	cytochrome-c oxida
311	311	74.5	5.4	293	2	AH3077	hypothetical prote	384	73.5	5.3	498	2	F89861	Na+/H+-antiporter
312	312	74.5	5.4	305	2	B33465	lic-1 protein B -	385	73.5	5.3	507	2	B97765	ADP-ATP carrier pr
313	313	74.5	5.4	311	2	F70184	ribose/galactose A	386	73.5	5.3	522	2	D86263	F13K23.21 protein
314	314	74.5	5.4	323	2	T31697	hypothetical prote	387	73.5	5.3	526	2	S74025	conserved hypothet
315	315	74.5	5.4	324	1	C47691	phospho-N-acetylm	388	73.5	5.3	527	2	T29433	hypothetical prote
316	316	74.5	5.4	325	2	F82558	lipopolysaccharide	389	73.5	5.3	546	2	AB2639	pH adaption potass
317	317	74.5	5.4	366	2	H86614	CT838 hypothetical	390	73.5	5.3	548	2	C97421	phad protein (X933
318	318	74.5	5.4	366	2	C72009	conserved hypothet	391	73.5	5.3	592	2	E75032	carbon starvation
319	319	74.5	5.4	367	2	T13813	NADH2 dehydrogenas	392	73.5	5.3	607	2	S19585	serotonin transpor
320	320	74.5	5.4	399	2	T27853	hypothetical prote	393	73.5	5.3	607	2	S63395	probable membrane
321	321	74.5	5.4	409	1	F69814	fosmidmycin resist	394	73.5	5.3	630	2	S30604	neurotransmitter t

395	73.5	5.3	674	2	E82954	conserved hypotet	468	72.5	5.2	741	2	T13085	NADH2 dehydrogenas
396	73.5	5.3	699	2	T13730	NADH2 dehydrogenas	469	72.5	5.2	743	2	T13073	NADH2 dehydrogenas
397	73.5	5.3	875	2	H93771	proteinase [import	470	72.5	5.2	744	2	T13040	NADH2 dehydrogenas
398	73.5	5.3	885	2	B69783	transporter homolo	471	72.5	5.2	744	2	T13757	NADH2 dehydrogenas
399	73.5	5.3	889	2	T20123	hypothetical prote	472	72.5	5.2	917	2	T17244	hypothetical prote
400	73.5	5.3	1099	2	A55405	adenylate cyclase	473	72.5	5.2	923	2	C97487	hypothetical prote
401	73.5	5.3	1128	2	T04922	hypothetical prote	474	72.5	5.2	923	2	AC2705	conserved hypotet
402	73.5	5.3	1343	2	AF0611	cell division prot	475	72.5	5.2	953	2	S54478	probable membrane
403	73.5	5.3	2818	2	B55282	neurofibromatosis-	476	72.5	5.2	958	2	A70634	probable mmp11 pro
404	73.5	5.3	2820	2	JC5196	neurofibromin I -	477	72.5	5.2	978	2	JC8067	mitochondrial Cl-t
405	73.5	5.3	2825	2	I54352	neurofibromin - mo	478	72.5	5.2	1148	2	H90175	NADH dehydrogenase
406	73	5.2	140	2	C83199	hypothetical prote	479	72.5	5.2	1329	2	A64828	cell division prot
407	73	5.2	193	2	B91170	hypothetical membr	480	72.5	5.2	2658	2	A86216	protein T23G18.2 l
408	73	5.2	193	2	B86016	hypothetical prote	481	72	5.2	215	2	F75166	hypothetical prote
409	73	5.2	261	2	AC0251	high-affinity zinc	482	72	5.2	242	2	S49598	membrane protein -
410	73	5.2	262	2	F97151	ABC transported MD	483	72	5.2	249	2	A71234	hypothetical prote
411	73	5.2	282	2	H71696	hypothetical prote	484	72	5.2	252	2	A71165	hypothetical prote
412	73	5.2	283	2	D83009	probable permease	485	72	5.2	257	2	AC1024	probable dimethyl
413	73	5.2	292	2	C95147	licB protein limpo	486	72	5.2	260	1	WVZP0	FP0 protein - fowl
414	73	5.2	294	2	D81434	probable 4-hydroxy	487	72	5.2	261	2	S62047	probable membrane
415	73	5.2	296	2	A98015	hypothetical prote	488	72	5.2	282	2	D98058	hypothetical prote
416	73	5.2	301	2	AH2064	hypothetical prote	489	72	5.2	286	2	T23066	hypothetical prote
417	73	5.2	311	2	T33436	hypothetical prote	490	72	5.2	315	2	B83778	ferrichrome ABC tr
418	73	5.2	364	2	D95959	conserved hypotet	491	72	5.2	339	2	E86761	conserved hypotet
419	73	5.2	384	2	S37608	NADH2 dehydrogenas	492	72	5.2	339	2	T23244	hypothetical prote
420	73	5.2	399	2	AE0396	probable sugar tra	493	72	5.2	355	2	A55733	G protein-coupled
421	73	5.2	401	2	T49929	hypothetical prote	494	72	5.2	359	2	AF3044	hypothetical prote
422	73	5.2	436	2	S77639	exopolysaccharide	495	72	5.2	361	2	C84246	ribose ABC transpo
423	73	5.2	437	2	D86633	amino acid permeas	496	72	5.2	367	2	C82943	ferrichrome ABC tr
424	73	5.2	453	2	AD1556	conserved hypotet	497	72	5.2	374	2	F98241	mtIK protein (AF00
425	73	5.2	456	2	H97735	hypothetical prote	498	72	5.2	378	2	T34372	hypothetical prote
426	73	5.2	470	2	B61118	transport of D-ala	499	72	5.2	417	2	F30916	probable transport
427	73	5.2	470	2	B91277	D-serine/D-alanine	500	72	5.2	417	2	F64915	membrane protein y
428	73	5.2	470	2	S56433	NADH2 dehydrogenas	501	72	5.2	421	2	C85765	probable transport
429	73	5.2	495	1	S25942	amino acid antipor	502	72	5.2	431	2	B84129	ammonium transport
430	73	5.2	507	2	AB1370	amino acid antipor	503	72	5.2	432	2	C82432	sugar transporter
431	73	5.2	574	2	T05964	probable low-affin	504	72	5.2	440	2	C82410	conserved hypotet
432	73	5.2	633	2	T13189	hypothetical prote	505	72	5.2	440	2	C75107	modulation protein
433	73	5.2	639	2	G88839	protein C10C6.5 [i	506	72	5.2	444	2	T24076	hypothetical prote
434	73	5.2	700	2	T13668	NADH2 dehydrogenas	507	72	5.2	447	2	AE0094	probable gluconate
435	73	5.2	732	2	T14233	NADH2 dehydrogenas	508	72	5.2	453	2	H71732	cytochrome D ubiqu
436	73	5.2	1564	2	T27121	hypothetical prote	509	72	5.2	463	2	H69822	sodium-glutamate s
437	73	5.2	3079	1	RGBY12	probable GTPase-ac	510	72	5.2	482	2	T17022	NADH2 dehydrogenas
438	73	5.2	3898	1	GNVH8	genome polypeptin	511	72	5.2	507	2	B71695	adp, ATP carrier p
439	72.5	5.2	118	2	G64394	hypothetical prote	512	72	5.2	524	2	AD1897	hypothetical prote
440	72.5	5.2	235	2	F95230	membrane protein [513	72	5.2	530	1	G64918	phosphotransferase
441	72.5	5.2	235	2	A93095	conserved hypotet	514	72	5.2	530	2	T51836	high affinity nitr
442	72.5	5.2	235	2	AF0598	probable membrane	515	72	5.2	582	2	H96604	probable 3'-5' exo
443	72.5	5.2	271	2	T11704	NADH2 dehydrogenas	516	72	5.2	602	2	AC2313	hypothetical prote
444	72.5	5.2	284	2	AH0680	probable dimethyl	517	72	5.2	608	2	S76192	hypothetical prote
445	72.5	5.2	286	2	B99213	cytochrome C oxida	518	72	5.2	614	2	T13727	NADH2 dehydrogenas
446	72.5	5.2	297	2	F82039	ribonuclease BN VC	519	72	5.2	620	2	F83976	cytochrome-c oxida
447	72.5	5.2	308	2	AF0461	probable membrane	520	72	5.2	628	2	AG2707	hypothetical prote
448	72.5	5.2	330	2	D95902	probable sugar ABC	521	72	5.2	629	2	H97489	mitochondrial tran
449	72.5	5.2	347	2	AD2201	hypothetical prote	522	72	5.2	641	2	AG2164	hypothetical prote
450	72.5	5.2	368	2	T13815	NADH2 dehydrogenas	523	72	5.2	644	2	B97885	transporter, trunc
451	72.5	5.2	375	2	B40205	Na+/H+-exchanging	524	72	5.2	681	2	T13566	NADH2 dehydrogenas
452	72.5	5.2	421	2	T22969	hypothetical prote	525	72	5.2	689	2	T11917	hypothetical prote
453	72.5	5.2	434	2	D65132	hypothetical 46.5	526	72	5.2	692	2	T33786	hypothetical prote
454	72.5	5.2	458	2	B90623	NADH dehydrogenase	527	72	5.2	696	2	T12160	NADH2 dehydrogenas
455	72.5	5.2	459	2	T19110	hypothetical prote	528	72	5.2	698	2	T12565	NADH2 dehydrogenas
456	72.5	5.2	461	2	G85059	probable sugar tra	529	72	5.2	698	2	T12161	NADH2 dehydrogenas
457	72.5	5.2	461	2	S75711	hypothetical prote	530	72	5.2	700	2	T13763	NADH2 dehydrogenas
458	72.5	5.2	491	2	H83979	lysine decarboxyla	531	72	5.2	719	2	T13793	NADH2 dehydrogenas
459	72.5	5.2	494	1	F69355	Na+/H+ antipoter	532	72	5.2	796	2	S62464	conserved hypotet
460	72.5	5.2	498	2	B89832	hypothetical prote	533	72	5.2	906	2	S35312	coatomer complex b
461	72.5	5.2	523	2	A11970	hypothetical prote	534	72	5.2	2150	2	T08165	RNA1 polyprotein -
462	72.5	5.2	615	2	S77084	ABC-type transporter	535	71.5	5.1	213	2	A71049	hypothetical prote
463	72.5	5.2	646	2	B70001	ABC transporter (p	536	71.5	5.1	232	2	E86825	hypothetical prote
464	72.5	5.2	682	2	T12715	NADH2 dehydrogenas	537	71.5	5.1	260	2	H89899	phosphatidate cyti
465	72.5	5.2	684	2	T13491	NADH2 dehydrogenas	538	71.5	5.1	281	2	A55862	aara protein - Pro
466	72.5	5.2	704	2	T13665	NADH2 dehydrogenas	539	71.5	5.1	283	2	B69769	hypothetical prote
467	72.5	5.2	736	2	T12716	NADH2 dehydrogenas	540	71.5	5.1	285	2	A11127	Staphylococcus xyl

541	71.5	5.1	295	2	AB0462	sn-glycerol-3-phos	614	71	5.1	468	2	D83625	probable transport
542	71.5	5.1	303	2	T32277	hypothetical prote	615	71	5.1	469	2	E86075	probable permease
543	71.5	5.1	308	2	H70767	hypothetical prote	616	71	5.1	478	2	A97079	MDR-type permease
544	71.5	5.1	323	2	G84003	DNA transport mach	617	71	5.1	492	2	D75188	proline symporter
545	71.5	5.1	324	2	F81018	iron(III) ABC tran	618	71	5.1	498	2	H81796	NADH2 dehydrogenas
546	71.5	5.1	337	2	F82214	galactoside ABC tr	619	71	5.1	502	1	ACHUA7	nicotinic acetylch
547	71.5	5.1	341	2	F82712	integral membrane	620	71	5.1	502	2	G02259	alpha 7 neuronal n
548	71.5	5.1	348	2	A82322	octaprenyl-diphosp	621	71	5.1	502	2	A57175	nicotinic acetylch
549	71.5	5.1	349	2	T31856	hypothetical prote	622	71	5.1	502	2	T01378	nicotinic receptor
550	71.5	5.1	373	2	A98094	type III secretion	623	71	5.1	509	2	A82840	beta-lactamase ind
551	71.5	5.1	373	2	E85939	hypothetical prote	624	71	5.1	541	2	D82302	iron(III) ABC tran
552	71.5	5.1	373	2	D71142	hypothetical prote	625	71	5.1	555	2	T24671	hypothetical prote
553	71.5	5.1	382	2	H85014	probable acetyltra	626	71	5.1	569	2	T00477	probable amino aci
554	71.5	5.1	391	2	A55119	potassium channel	627	71	5.1	579	2	AB1414	ABC transporter (A
555	71.5	5.1	406	2	C86904	transporter yxbd [628	71	5.1	593	2	A10559	probable ABC trans
556	71.5	5.1	418	2	H97763	proline/betaine tr	629	71	5.1	594	2	A49804	cellular Hsp70 hom
557	71.5	5.1	432	2	D95369	conserved hypotet	630	71	5.1	612	2	S74936	sulfur deprivation
558	71.5	5.1	445	2	T20190	hypothetical prote	631	71	5.1	684	2	T12151	NADH2 dehydrogenas
559	71.5	5.1	470	2	A69751	histidine permease	632	71	5.1	685	2	T12138	NADH2 dehydrogenas
560	71.5	5.1	470	2	C70554	hypothetical prote	633	71	5.1	686	2	T12128	NADH2 dehydrogenas
561	71.5	5.1	477	2	F86670	lysine specific pe	634	71	5.1	688	2	T13237	NADH2 dehydrogenas
562	71.5	5.1	497	2	G81598	serine hydroxymeth	635	71	5.1	688	2	T13249	NADH2 dehydrogenas
563	71.5	5.1	506	2	F88954	protein K04F1.14 [636	71	5.1	698	2	T12560	NADH2 dehydrogenas
564	71.5	5.1	512	2	S75887	hypothetical prote	637	71	5.1	699	2	T12648	NADH2 dehydrogenas
565	71.5	5.1	519	2	E86555	serine hydroxymeth	638	71	5.1	704	2	T13729	NADH2 dehydrogenas
566	71.5	5.1	519	2	H72067	glycine hydroxymet	639	71	5.1	737	2	T13067	NADH2 dehydrogenas
567	71.5	5.1	532	2	S59087	cytochrome-c oxida	640	71	5.1	918	2	A36337	membrane glycoprot
568	71.5	5.1	532	2	S66087	amino acid transpo	641	71	5.1	1506	2	T51900	related to PAN2 pr
569	71.5	5.1	533	2	H69326	conserved hypotet	642	70.5	5.1	133	2	A13582	hypothetical prote
570	71.5	5.1	534	2	C87023	probable cell divi	643	70.5	5.1	167	2	T20548	hypothetical prote
571	71.5	5.1	539	2	S77595	cytochrome-c oxida	644	70.5	5.1	175	2	T39999	hypothetical prote
572	71.5	5.1	654	2	H89871	hypothetical prote	645	70.5	5.1	210	2	F64609	conserved hypotet
573	71.5	5.1	663	2	AG2696	cytochrome c-type	646	70.5	5.1	217	2	S76538	hypothetical prote
574	71.5	5.1	663	2	G97478	cytochrome c-type	647	70.5	5.1	234	2	C64815	ybmW protein - Esc
575	71.5	5.1	665	2	B96668	probable acyl-CoA	648	70.5	5.1	253	2	F75067	hypothetical prote
576	71.5	5.1	672	2	AF3084	conserved hypotet	649	70.5	5.1	263	2	T29414	hypothetical prote
577	71.5	5.1	672	2	C98202	hypothetical prote	650	70.5	5.1	263	2	T04051	hypothetical prote
578	71.5	5.1	696	2	B87265	Kup system potassi	651	70.5	5.1	267	2	H72590	hypothetical prote
579	71.5	5.1	698	2	T12590	NADH2 dehydrogenas	652	70.5	5.1	285	2	T12435	probable plasma me
580	71.5	5.1	718	1	B64040	hypothetical prote	653	70.5	5.1	285	2	D87209	probable transmemb
581	71.5	5.1	730	2	T12224	NADH2 dehydrogenas	654	70.5	5.1	286	2	T02451	plasma membrane in
582	71.5	5.1	741	2	T12642	NADH2 dehydrogenas	655	70.5	5.1	288	2	S41194	transmembrane prot
583	71.5	5.1	741	2	T12701	NADH2 dehydrogenas	656	70.5	5.1	290	2	A69779	conserved hypotet
584	71.5	5.1	746	2	T13678	NADH2 dehydrogenas	657	70.5	5.1	297	2	G69357	hypothetical prote
585	71.5	5.1	756	2	T04187	subtilisin-like pr	658	70.5	5.1	312	2	AB0306	probable membrane
586	71.5	5.1	765	2	F97186	probable cell wall	659	70.5	5.1	315	1	C69763	ferrichrome ABC tr
587	71.5	5.1	770	2	T23999	hypothetical prote	660	70.5	5.1	315	2	C81962	probable inner mem
588	71.5	5.1	854	2	D82324	conserved hypotet	661	70.5	5.1	318	2	E71054	probable sodium de
589	71.5	5.1	1067	2	AB0260	probable phage hos	662	70.5	5.1	327	2	D75196	hypothetical prote
590	71.5	5.1	1679	2	T50091	yeast Ecm29 cell w	663	70.5	5.1	346	2	AB0187	probable iron-side
591	71	5.1	200	1	F45456	NADH2 dehydrogenas	664	70.5	5.1	349	2	T33948	hypothetical prote
592	71	5.1	228	2	AE2541	hypothetical prote	665	70.5	5.1	358	2	T22823	hypothetical prote
593	71	5.1	229	2	A64137	molybdenum transpo	666	70.5	5.1	386	2	E89765	branched chain ami
594	71	5.1	243	2	B86740	lipopolysaccharide	667	70.5	5.1	387	2	AE1062	hypothetical prote
595	71	5.1	260	2	T30669	probable trans-act	668	70.5	5.1	394	2	C81333	probable efflux pu
596	71	5.1	260	2	C82116	flagellar biosynth	669	70.5	5.1	408	2	B42290	probable membrane
597	71	5.1	261	2	H69217	hypothetical prote	670	70.5	5.1	419	2	B90033	hypothetical prote
598	71	5.1	272	2	T11689	NADH2 dehydrogenas	671	70.5	5.1	430	2	A95935	conserved hypotet
599	71	5.1	297	2	AD2318	transcription regu	672	70.5	5.1	434	2	T15799	hypothetical prote
600	71	5.1	305	2	E90461	hypothetical prote	673	70.5	5.1	443	2	D71058	hypothetical prote
601	71	5.1	316	2	AB2931	hypothetical prote	674	70.5	5.1	446	2	B99284	conserved hypotet
602	71	5.1	316	2	D98351	dipeptide ABC tran	675	70.5	5.1	457	2	A83677	sodium-dependent t
603	71	5.1	333	2	T41669	hypothetical prote	676	70.5	5.1	458	2	B90615	NADH dehydrogenase
604	71	5.1	364	2	H83787	hypothetical prote	677	70.5	5.1	474	2	T38737	probable CAAX pren
605	71	5.1	396	1	E64143	chloramphenicol re	678	70.5	5.1	480	2	S39978	scrA protein - Sta
606	71	5.1	397	2	G95221	hypothetical prote	679	70.5	5.1	491	2	AC1499	transmembrane prot
607	71	5.1	397	2	T00098	hypothetical prote	680	70.5	5.1	507	2	AB1707	glycine betaine tr
608	71	5.1	397	2	B98085	hypothetical prote	681	70.5	5.1	507	2	B64433	probable O-antigen
609	71	5.1	448	2	T30982	hypothetical prote	682	70.5	5.1	508	2	D81325	probable phosphate
610	71	5.1	458	2	AF0631	probable 4-hydroxy	683	70.5	5.1	533	2	S51171	amino acid transpo
611	71	5.1	461	2	S60253	sel-12 protein - C	684	70.5	5.1	585	2	C82955	probable sodium/pr
612	71	5.1	466	2	E90046	hypothetical prote	685	70.5	5.1	593	2	JT0974	cytochrome-c oxida
613	71	5.1	468	2	I64182	Na+/H+-exchanging	686	70.5	5.1	593	2	F84223	cytochrome-c oxida

687	70.5	5.1	674	2	AC1913	two-component sens	760	70	5.0	2201	1	GNNYA9	genome polyprotein
688	70.5	5.1	683	2	T12158	NADH2 dehydrogenas	761	69.5	5.0	202	2	F86347	hypothetical prote
689	70.5	5.1	704	2	T13581	NADH2 dehydrogenas	762	69.5	5.0	210	2	H81406	probable integral
690	70.5	5.1	718	2	S48726	phenylalanine ammo	763	69.5	5.0	215	2	S75345	hypothetical prote
691	70.5	5.1	733	2	T12213	NADH2 dehydrogenas	764	69.5	5.0	222	2	E72228	hypothetical prote
692	70.5	5.1	737	2	T13504	NADH2 dehydrogenas	765	69.5	5.0	224	2	B71191	hypothetical prote
693	70.5	5.1	738	2	C95936	conserved hypothet	766	69.5	5.0	256	2	S26742	tonoplast intrinsi
694	70.5	5.1	740	1	DENTN5	NADH2 dehydrogenas	767	69.5	5.0	260	2	G64690	type IIS restricti
695	70.5	5.1	741	2	T12610	NADH2 dehydrogenas	768	69.5	5.0	265	2	AF2007	hypothetical prote
696	70.5	5.1	741	2	T12702	NADH2 dehydrogenas	769	69.5	5.0	268	2	A70417	hypothetical prote
697	70.5	5.1	741	2	T13233	NADH2 dehydrogenas	770	69.5	5.0	285	1	C32804	prephenate dehydra
698	70.5	5.1	741	2	T13569	NADH2 dehydrogenas	771	69.5	5.0	285	1	AE1488	Staphylococcus xyl
699	70.5	5.1	921	2	T19694	hypothetical prote	772	69.5	5.0	286	2	F87075	membrane transport
700	70.5	5.1	1134	2	A41350	adenylate cyclase	773	69.5	5.0	287	2	T09791	drought-induced ma
701	70.5	5.1	1681	2	A55138	sodium channel mNa	774	69.5	5.0	292	2	G52888	hypothetical prote
702	70.5	5.1	1781	1	A43374	DNA-directed RNA p	775	69.5	5.0	294	2	S76277	ycf38 protein - Sy
703	70.5	5.1	2143	2	G96595	hypothetical prote	776	69.5	5.0	308	2	S16648	dipeptide transport
704	70	5.0	98	2	T17099	NADH2 dehydrogenas	777	69.5	5.0	315	2	F72374	conserved hypothet
705	70	5.0	160	2	F72322	hypothetical prote	778	69.5	5.0	317	2	S72851	hypothetical prote
706	70	5.0	169	2	AB2739	acetyltransferase	779	69.5	5.0	325	2	T14227	NADH2 dehydrogenas
707	70	5.0	209	2	H97519	hypothetical prote	780	69.5	5.0	329	2	T11350	NADH2 dehydrogenas
708	70	5.0	240	1	Q0BEG3	HMLF4 protein - hu	781	69.5	5.0	334	2	T19955	hypothetical prote
709	70	5.0	245	2	A90527	hypothetical prote	782	69.5	5.0	340	2	AE0353	probable membrane
710	70	5.0	250	2	C91020	hypothetical prote	783	69.5	5.0	351	2	T11794	NADH2 dehydrogenas
711	70	5.0	251	2	AH0575	2,3-dihydro-2,3-di	784	69.5	5.0	353	2	S65297	probable membrane
712	70	5.0	254	2	B70235	hypothetical prote	785	69.5	5.0	358	2	T29744	hypothetical prote
713	70	5.0	273	2	A72378	conserved hypothet	786	69.5	5.0	371	2	H97452	cytochrome c oxida
714	70	5.0	282	2	A92025	hypothetical prote	787	69.5	5.0	372	2	G82790	hypothetical prote
715	70	5.0	287	2	T12440	mipC protein - com	788	69.5	5.0	385	2	AE2717	permease [imported
716	70	5.0	320	2	T20176	hypothetical prote	789	69.5	5.0	385	2	H97498	permease AGR_C 211
717	70	5.0	325	2	C98135	hypothetical prote	790	69.5	5.0	393	1	A48357	nonstructural prot
718	70	5.0	325	2	AH3152	hypothetical prote	791	69.5	5.0	398	2	C90349	multidrug-efflux t
719	70	5.0	344	2	AE3228	agrocinopine synth	792	69.5	5.0	415	2	A39412	tryptophan transpo
720	70	5.0	344	2	S51948	hypothetical prote	793	69.5	5.0	420	2	AE2458	hypothetical prote
721	70	5.0	345	2	H95381	probable iron upta	794	69.5	5.0	426	2	E86575	phosphate permease
722	70	5.0	397	2	AP2016	hypothetical prote	795	69.5	5.0	439	2	A64769	branched-chain ami
723	70	5.0	413	2	H81659	branched-chain ami	796	69.5	5.0	439	2	C90685	branched-chain ami
724	70	5.0	427	2	S74444	hypothetical prote	797	69.5	5.0	439	2	G85535	branched-chain ami
725	70	5.0	442	2	E85864	probable transport	798	69.5	5.0	440	2	H90253	NADH-Ubiquinone/pl
726	70	5.0	443	2	H85485	probable transport	799	69.5	5.0	443	2	AG1335	hypothetical prote
727	70	5.0	443	2	H90634	probable transport	800	69.5	5.0	448	2	A69747	ABC transporter (p
728	70	5.0	456	2	F97810	magnesium transport	801	69.5	5.0	458	2	B81409	probable transmemb
729	70	5.0	458	2	A37869	alpha-2B-adrenergi	802	69.5	5.0	459	2	S10196	NADH2 dehydrogenas
730	70	5.0	459	2	T11110	NADH2 dehydrogenas	803	69.5	5.0	470	2	C87683	conserved hypothet
731	70	5.0	459	2	S28025	light harvesting c	804	69.5	5.0	472	2	B91091	L-arabinose isomer
732	70	5.0	467	2	F91228	probable permease	805	69.5	5.0	472	2	E85936	L-arabinose isomer
733	70	5.0	503	2	AB2734	NADH dehydrogenase	806	69.5	5.0	472	2	B26430	L-arabinose isomer
734	70	5.0	503	2	D97515	NADH dehydrogenase	807	69.5	5.0	475	2	E83450	cytochrome-c oxida
735	70	5.0	519	2	F84222	quinone oxidoreduc	808	69.5	5.0	475	2	D83128	cytochrome-c oxida
736	70	5.0	522	2	B83987	ABC transporter (p	809	69.5	5.0	478	2	AC3395	NADH2 dehydrogenas
737	70	5.0	539	2	E97025	spoVB related memb	810	69.5	5.0	482	2	T45295	cytochrome-c oxida
738	70	5.0	539	2	S67049	probable membrane	811	69.5	5.0	493	2	S52421	amino acid transpo
739	70	5.0	576	2	B71420	hypothetical prote	812	69.5	5.0	507	2	T48645	glycine betaine tr
740	70	5.0	600	2	T32343	hypothetical prote	813	69.5	5.0	507	2	AD1336	glycine betaine tr
741	70	5.0	614	2	B84949	NADH2 dehydrogenas	814	69.5	5.0	515	2	T03717	GTP-binding protei
742	70	5.0	658	2	B86599	metal transport P-	815	69.5	5.0	536	2	A71491	probable integral
743	70	5.0	658	2	D72026	metal transport P-	816	69.5	5.0	570	2	S42708	proline transport
744	70	5.0	670	2	JQ1447	NADH2 dehydrogenas	817	69.5	5.0	570	2	S04547	proline transport
745	70	5.0	683	2	C81515	cation-transportin	818	69.5	5.0	572	2	AB2671	cytochrome-c oxida
746	70	5.0	688	2	T12670	NADH2 dehydrogenas	819	69.5	5.0	591	2	S14115	NADH2 dehydrogenas
747	70	5.0	698	2	T12556	NADH2 dehydrogenas	820	69.5	5.0	591	2	S43506	hypothetical prote
748	70	5.0	700	2	T13702	NADH2 dehydrogenas	821	69.5	5.0	615	2	S77332	NADH2 dehydrogenas
749	70	5.0	705	2	T13494	NADH2 dehydrogenas	822	69.5	5.0	627	2	T11125	NADH2 dehydrogenas
750	70	5.0	732	2	T12194	NADH2 dehydrogenas	823	69.5	5.0	627	2	S67257	proline transport
751	70	5.0	738	2	T14230	NADH2 dehydrogenas	824	69.5	5.0	631	2	S75742	hypothetical prote
752	70	5.0	744	2	A81719	exodeoxyribonuclea	825	69.5	5.0	643	2	S70592	NADH2 dehydrogenas
753	70	5.0	782	2	T25925	hypothetical prote	826	69.5	5.0	654	2	T14202	NADH2 dehydrogenas
754	70	5.0	836	2	B89453	adenylate cyclase	827	69.5	5.0	686	2	T13680	NADH2 dehydrogenas
755	70	5.0	860	2	AB2044	adenylate cyclase	828	69.5	5.0	701	2	T12296	NADH2 dehydrogenas
756	70	5.0	1018	2	T19693	hypothetical prote	829	69.5	5.0	718	2	A99195	hypothetical prote
757	70	5.0	1070	2	B86922	probable arabinosy	830	69.5	5.0	736	2	T12214	NADH2 dehydrogenas
758	70	5.0	1155	2	B71720	hypothetical prote	831	69.5	5.0	741	2	T12706	NADH2 dehydrogenas
759	70	5.0	2108	2	S72458	sodium channel pro	832	69.5	5.0	741	2	T13086	NADH2 dehydrogenas

833	69.5	5.0	741	2	T13372	NADH2 dehydrogenas	906	69	5.0	670	1	DNOB5	NADH2 dehydrogenas
834	69.5	5.0	744	2	T13682	NADH2 dehydrogenas	907	69	5.0	677	2	T11231	NADH2 dehydrogenas
835	69.5	5.0	747	2	E91049	probable cytochrom	908	69	5.0	684	2	T13695	NADH2 dehydrogenas
836	69.5	5.0	747	2	A85894	probable cytochrom	909	69	5.0	691	2	T12293	NADH2 dehydrogenas
837	69.5	5.0	809	1	S5BYQT	glutamine-tRNA lig	910	69	5.0	692	2	H71494	probable thiol-dis
838	69.5	5.0	970	2	A13605	potassium efflux s	911	69	5.0	702	2	T13505	NADH2 dehydrogenas
839	69.5	5.0	1302	2	B41249	multidrug resistanc	912	69	5.0	724	2	B83342	NADH2 dehydrogenas
840	69.5	5.0	1645	2	T13339	carbamoyl-phosphat	913	69	5.0	737	2	T12193	NADH2 dehydrogenas
841	69.5	5.0	1827	2	A35694	cut1 protein - fis	914	69	5.0	777	2	AF2410	serine/threonine k
842	69.5	5.0	1828	2	T41455	cut1 protein - fis	915	69	5.0	903	2	A10015	malonate regulon po
843	69	5.0	139	2	T31033	hypothetical prote	916	69	5.0	904	2	A84212	hypothetical prote
844	69	5.0	171	2	AF4434	hypothetical prote	917	69	5.0	975	2	T22788	hypothetical prote
845	69	5.0	233	2	S77443	cytochrome-c oxida	918	68.5	4.9	179	2	AD2573	hypothetical prote
846	69	5.0	233	2	AH1068	probable membrane	919	68.5	4.9	218	2	AE1473	hypothetical prote
847	69	5.0	236	2	S42069	TEGT protein - rat	920	68.5	4.9	272	2	T11550	probable membrane
848	69	5.0	254	2	C84315	hypothetical prote	921	68.5	4.9	289	2	D87933	protein R06C1.2 [i
849	69	5.0	260	2	AG0434	probable membrane	922	68.5	4.9	295	2	T01528	probable plasma me
850	69	5.0	281	2	D64426	phosphate transpor	923	68.5	4.9	296	2	E69025	conserved hypothet
851	69	5.0	288	2	H72092	prolipoprotein dia	924	68.5	4.9	303	2	AG1396	cation transport p
852	69	5.0	288	2	G86529	prolipoprotein dia	925	68.5	4.9	305	2	S66005	conserved hypothet
853	69	5.0	290	2	T09260	aquaporin-like tra	926	68.5	4.9	313	2	C71545	probable oligopept
854	69	5.0	292	2	D81575	prolipoprotein tra	927	68.5	4.9	333	2	S52960	NADH2 dehydrogenas
855	69	5.0	296	1	BVRCPT	phosphate transpor	928	68.5	4.9	336	2	I64096	transmembrane pore
856	69	5.0	296	2	F91211	hypothetical prote	929	68.5	4.9	346	2	B98135	hypothetical prote
857	69	5.0	296	2	F86057	hypothetical prote	930	68.5	4.9	346	2	A13152	hypothetical prote
858	69	5.0	299	2	T06960	probable membrane	931	68.5	4.9	347	2	G96741	unknown protein F1
859	69	5.0	305	2	F70030	conserved hypothet	932	68.5	4.9	352	2	T23962	hypothetical prote
860	69	5.0	308	2	C86561	phosphatidate cyti	933	68.5	4.9	365	2	C97088	spore germination
861	69	5.0	308	2	H72062	phosphatidate cyti	934	68.5	4.9	367	2	T14228	NADH2 dehydrogenas
862	69	5.0	313	2	H71341	conserved hypothet	935	68.5	4.9	372	2	AB0276	probable membrane
863	69	5.0	347	2	T29415	hypothetical prote	936	68.5	4.9	383	2	C83436	probable MFS metab
864	69	5.0	364	2	D96973	spore germination	937	68.5	4.9	401	2	G95968	probable transport
865	69	5.0	369	2	F69478	NADH2 dehydrogenas	938	68.5	4.9	407	2	A69188	ammonium transport
866	69	5.0	387	2	E83679	multidrug-efflux t	939	68.5	4.9	454	2	AE1244	acetyl-CoA carboxy
867	69	5.0	389	2	T51355	membrane protein [940	68.5	4.9	454	2	A11606	acetyl-CoA carboxy
868	69	5.0	391	2	AB1285	transmembrane tran	941	68.5	4.9	455	2	F97065	D-xylose-proton sy
869	69	5.0	396	2	F83130	probable MFS trans	942	68.5	4.9	459	2	B95009	potassium uptake p
870	69	5.0	397	2	E81223	conserved hypothet	943	68.5	4.9	459	2	F97880	hypothetical prote
871	69	5.0	397	2	B81994	probable transmemb	944	68.5	4.9	462	2	H81952	probable integral
872	69	5.0	411	2	F97088	sugar-proton sympo	945	68.5	4.9	468	2	AE2163	hypothetical prote
873	69	5.0	416	2	C81324	ubiquinol-cytochro	946	68.5	4.9	475	2	C83452	cytochrome-c oxida
874	69	5.0	429	2	A10792	probable transport	947	68.5	4.9	487	2	E97747	NADH2 dehydrogenas
875	69	5.0	431	2	A84380	hypothetical prote	948	68.5	4.9	488	1	OXASB1	mrna maturase bil
876	69	5.0	432	2	C85087	hypothetical prote	949	68.5	4.9	489	2	E89102	protein F25E5.11 [
877	69	5.0	443	2	E64725	yaau protein - Eac	950	68.5	4.9	507	2	B69316	DNA gyrase, subuni
878	69	5.0	449	2	AE1707	PTS system galacti	951	68.5	4.9	509	2	T41034	probable WD-domain
879	69	5.0	451	2	E81781	probable integral	952	68.5	4.9	537	2	A11277	probable transport
880	69	5.0	451	2	AB1206	sugar transporter,	953	68.5	4.9	546	2	G86440	hypothetical prote
881	69	5.0	455	2	B90619	NADH dehydrogenase	954	68.5	4.9	597	2	T41501	major facilitator
882	69	5.0	458	2	B96643	hypothetical prote	955	68.5	4.9	616	2	F90371	amino acid transpo
883	69	5.0	462	2	D86814	transport protein	956	68.5	4.9	627	2	C96981	ABC transporter AT
884	69	5.0	464	2	C40630	GDP-mannose pyroph	957	68.5	4.9	637	2	AC3217	potassium uptake p
885	69	5.0	473	2	T03611	cyclin, B-type - c	958	68.5	4.9	685	2	T12129	NADH2 dehydrogenas
886	69	5.0	478	2	T29174	hypothetical prote	959	68.5	4.9	687	2	T12126	NADH2 dehydrogenas
887	69	5.0	482	2	C90067	hypothetical prote	960	68.5	4.9	688	2	T13242	NADH2 dehydrogenas
888	69	5.0	483	2	AB1352	integral membrane	961	68.5	4.9	688	2	T13373	NADH2 dehydrogenas
889	69	5.0	487	2	S40820	probable permease	962	68.5	4.9	689	2	T13681	NADH2 dehydrogenas
890	69	5.0	488	1	H64537	cytochrome-c oxida	963	68.5	4.9	698	2	T13492	NADH2 dehydrogenas
891	69	5.0	488	2	G71969	cytochrome-c oxida	964	68.5	4.9	701	2	F70155	Na+/H+ antiporter
892	69	5.0	492	2	AD3055	succinoglycan bios	965	68.5	4.9	716	2	E82016	probable integral
893	69	5.0	495	2	S75340	NADH2 dehydrogenas	966	68.5	4.9	721	2	B83820	hypothetical prote
894	69	5.0	498	2	H82494	probable NADH dehy	967	68.5	4.9	736	2	T12225	NADH2 dehydrogenas
895	69	5.0	509	2	D86978	hypothetical prote	968	68.5	4.9	736	2	T12222	NADH2 dehydrogenas
896	69	5.0	516	2	G82182	probable NADH dehy	969	68.5	4.9	741	2	T12711	NADH2 dehydrogenas
897	69	5.0	522	2	A98231	succinoglycan bios	970	68.5	4.9	741	2	T12620	NADH2 dehydrogenas
898	69	5.0	528	2	T34941	probable Na+/H+ an	971	68.5	4.9	741	2	T12699	NADH2 dehydrogenas
899	69	5.0	554	2	S03809	cytochrome-c oxida	972	68.5	4.9	743	2	T13700	NADH2 dehydrogenas
900	69	5.0	588	2	A43740	DG42 protein - Afr	973	68.5	4.9	743	2	T12760	NADH2 dehydrogenas
901	69	5.0	591	2	G97748	virD4 protein [imp	974	68.5	4.9	744	2	T12705	NADH2 dehydrogenas
902	69	5.0	605	2	H95240	conserved hypothet	975	68.5	4.9	745	2	G84995	vacB protein [impo
903	69	5.0	605	2	A99705	hypothetical prote	976	68.5	4.9	746	2	C95110	competence protein
904	69	5.0	642	2	T33262	hypothetical prote	977	68.5	4.9	747	2	T13683	NADH2 dehydrogenas
905	69	5.0	652	2	C97087	probable permease	978	68.5	4.9	750	2	B90137	sulfate permease [

979	68.5	4.9	820	2	D71471	probable DNA misma	1052	68	4.9	899	2	S76449	hypothetical prote
980	68.5	4.9	827	2	A95877	hypothetical prote	1053	68	4.9	906	2	S35342	Golgi-associated p
981	68.5	4.9	870	2	A83201	protein F32D8.4 [i	1054	68	4.9	909	2	F72453	probable cytochrom
982	68.5	4.9	874	2	JQ0883	genome polyprotein	1055	68	4.9	1039	2	C87083	C-term lyse1-trNA
983	68.5	4.9	881	2	AE2777	potassium efflux s	1056	68	4.9	1082	2	T45096	probable arabinosy
984	68.5	4.9	881	2	B97557	hypothetical prote	1057	68	4.9	1323	2	T18214	ATP binding casset
985	68.5	4.9	912	2	T21659	hypothetical prote	1058	68	4.9	1368	2	T51622	probable aldehyde
986	68.5	4.9	960	2	A82142	probable cell divi	1059	68	4.9	1541	1	S71839	canalicular multidi
987	68.5	4.9	1081	2	T52028	cellulose synthase	1060	67.5	4.8	100	2	B69836	hypothetical prote
988	68.5	4.9	1084	2	T08583	cellulose synthase	1061	67.5	4.8	212	2	A11111	hypothetical prote
989	68.5	4.9	1394	2	S66876	ATP-dependent tran	1062	67.5	4.8	269	2	E72693	hypothetical prote
990	68.5	4.9	1504	2	A33602	DNA-directed DNA p	1063	67.5	4.8	284	2	AC1198	Streptococcus agal
991	68	4.9	148	2	S74589	hypothetical prote	1064	67.5	4.8	288	2	T33224	hypothetical prote
992	68	4.9	183	2	T49855	hypothetical prote	1065	67.5	4.8	291	2	B95316	probable ABC trans
993	68	4.9	214	2	G83882	hypothetical prote	1066	67.5	4.8	293	2	D81673	ABC transporter, p
994	68	4.9	215	2	S16564	noH protein - Rhi	1067	67.5	4.8	300	2	G70943	hypothetical prote
995	68	4.9	237	2	H86841	transport permease	1068	67.5	4.8	302	2	G90078	hypothetical prote
996	68	4.9	241	2	T33804	hypothetical prote	1069	67.5	4.8	302	2	G71660	hypothetical prote
997	68	4.9	252	2	A70529	hypothetical prote	1070	67.5	4.8	302	2	AF2686	ABC transporter, m
998	68	4.9	254	2	E70438	type 4 prepilin pe	1071	67.5	4.8	302	2	C97468	probable permease
999	68	4.9	256	2	C72261	spermidine/putresc	1072	67.5	4.8	304	2	AD1029	probable membrane
1000	68	4.9	265	2	AD0214	PTS system, mannos	1073	67.5	4.8	307	2	C70952	probable sugA prot
1001	68	4.9	265	2	E82716	ATP synthase, A ch	1074	67.5	4.8	310	2	A86812	sugar ABC transpor
1002	68	4.9	282	2	AD0848	iron transport pro	1075	67.5	4.8	314	2	AB2230	hypothetical prote
1003	68	4.9	286	2	D83914	chloramphenicol re	1076	67.5	4.8	323	2	T31828	hypothetical prote
1004	68	4.9	296	2	AD0956	phosphate transpor	1077	67.5	4.8	327	1	S45529	NADPH2:quinone red
1005	68	4.9	304	2	A89905	hypothetical prote	1078	67.5	4.8	327	2	S67168	probable membrane
1006	68	4.9	312	2	F70044	hypothetical prote	1079	67.5	4.8	344	2	T32600	hypothetical prote
1007	68	4.9	316	2	S50336	NADH2 dehydrogenas	1080	67.5	4.8	347	2	T28733	hypothetical prote
1008	68	4.9	316	2	E81321	probable cation tr	1081	67.5	4.8	349	2	S51267	probable galactosy
1009	68	4.9	329	2	F98334	SN-glycerol 3-phos	1082	67.5	4.8	359	2	I51372	angiotensin II rec
1010	68	4.9	335	2	S44635	f22b7.7 protein -	1083	67.5	4.8	361	2	D72384	conserved hypotet
1011	68	4.9	353	2	T06515	probable adenosylm	1084	67.5	4.8	364	1	S77360	cbid protein - Syn
1012	68	4.9	357	2	C97744	hypothetical prote	1085	67.5	4.8	367	2	T32390	hypothetical prote
1013	68	4.9	358	2	T38914	para-hydroxybenzoa	1086	67.5	4.8	374	2	C91198	EsPD protein limpo
1014	68	4.9	396	2	AF0677	probable membrane	1087	67.5	4.8	374	2	G86044	secreted protein E
1015	68	4.9	396	2	A91019	probable antibioti	1088	67.5	4.8	377	2	T21170	hypothetical prote
1016	68	4.9	396	2	C85863	probable antibioti	1089	67.5	4.8	379	2	D81515	cell shape-determi
1017	68	4.9	397	2	G90013	hypothetical prote	1090	67.5	4.8	387	2	J50364	lactosylceramide a
1018	68	4.9	408	2	AC1373	conserved hypotet	1091	67.5	4.8	393	2	T12608	NADH2 dehydrogenas
1019	68	4.9	417	2	E82966	tryptophan permeas	1092	67.5	4.8	402	2	B69843	conserved hypotet
1020	68	4.9	437	1	F64614	conserved hypotet	1093	67.5	4.8	409	2	AF3271	probable allantoin
1021	68	4.9	442	2	H81402	probable integral	1094	67.5	4.8	415	2	F91209	low affinity trypt
1022	68	4.9	448	2	G70172	conserved hypotet	1095	67.5	4.8	415	2	A86056	rod shape trypt
1023	68	4.9	461	2	H82186	probable multidrug	1096	67.5	4.8	415	2	A86599	rod shape protein
1024	68	4.9	469	2	C69628	gamma-aminobutyrat	1097	67.5	4.8	415	2	C72026	rod shape protein
1025	68	4.9	476	2	D83600	probable aldehyde	1098	67.5	4.8	415	2	H71841	hypothetical prote
1026	68	4.9	485	2	T24115	hypothetical prote	1099	67.5	4.8	426	2	A96000	probable C4-dicarb
1027	68	4.9	488	1	QXASM4	NADH2 dehydrogenas	1100	67.5	4.8	456	2	E83750	gluconate permease
1028	68	4.9	489	2	B53153	glucose transport	1101	67.5	4.8	456	2	B83391	probable amino aci
1029	68	4.9	494	2	JC2382	sodium/proline sym	1102	67.5	4.8	459	2	S47879	NADH2 dehydrogenas
1030	68	4.9	505	2	B97747	NADH2 dehydrogenas	1103	67.5	4.8	462	2	D81010	conserved hypotet
1031	68	4.9	512	2	G90399	amino acid transpo	1104	67.5	4.8	463	2	A69905	conserved hypotet
1032	68	4.9	521	2	E64181	probable cytochrom	1105	67.5	4.8	463	2	E83242	probable adenylate
1033	68	4.9	523	2	T12198	sucrose transport	1106	67.5	4.8	467	2	AB2493	hypothetical prote
1034	68	4.9	534	2	S64593	probable membrane	1107	67.5	4.8	467	2	AB1263	probable integral
1035	68	4.9	537	2	AH1640	probable transport	1108	67.5	4.8	477	2	D83617	probable amino aci
1036	68	4.9	550	2	T37519	probable amino aci	1109	67.5	4.8	483	2	A10449	protein-Npi-phosph
1037	68	4.9	564	2	C83742	cytochrome c oxida	1110	67.5	4.8	486	2	F71683	NADH2 dehydrogenas
1038	68	4.9	592	2	E70488	cytochrome-c oxida	1111	67.5	4.8	490	2	E82740	C4-dicarboxylate t
1039	68	4.9	593	2	S26696	alkaline proteinas	1112	67.5	4.8	495	2	B81297	sodium/proline sym
1040	68	4.9	600	2	C69371	conserved hypotet	1113	67.5	4.8	501	2	T02134	hypothetical prote
1041	68	4.9	602	2	T13679	NADH2 dehydrogenas	1114	67.5	4.8	510	2	H87320	conserved hypotet
1042	68	4.9	617	2	F82744	ferrous iron trans	1115	67.5	4.8	512	2	S28663	cytochrome-c oxida
1043	68	4.9	633	2	I58140	glycine transporte	1116	67.5	4.8	513	2	I45456	NADH2 dehydrogenas
1044	68	4.9	633	2	S45877	uracil transport p	1117	67.5	4.8	514	2	T46131	4-coumarate-CoA li
1045	68	4.9	638	2	JH0673	glycine transport	1118	67.5	4.8	519	1	S02153	NADH2 dehydrogenas
1046	68	4.9	683	2	T12295	NADH2 dehydrogenas	1119	67.5	4.8	552	2	E70731	probable pitB prot
1047	68	4.9	688	2	T12278	NADH2 dehydrogenas	1120	67.5	4.8	560	2	F81423	L-lactate permease
1048	68	4.9	689	2	T13762	NADH2 dehydrogenas	1121	67.5	4.8	568	2	JC7911	Na+-coupled citrat
1049	68	4.9	705	2	T12152	NADH2 dehydrogenas	1122	67.5	4.8	615	2	H82635	hypothetical prote
1050	68	4.9	709	2	A97218	uncharacterized co	1123	67.5	4.8	617	2	B82285	protein-export mem
1051	68	4.9	811	2	T36581	probable transmemb	1124	67.5	4.8	631	2	H70754	probable abc trans

1125	67.5	4.8	637	2	JH0674	L-proline transpor	1198	67	4.8	406	2	H89006	protein T22F3.11 [
1126	67.5	4.8	645	2	T12159	NADH2 dehydrogenas	1199	67	4.8	407	2	AD0706	O-antigen polymera
1127	67.5	4.8	645	2	A75390	NADH2 dehydrogenas	1200	67	4.8	407	2	A43672	O-antigen polymera
1128	67.5	4.8	659	2	T33557	hypothetical prote	1201	67	4.8	409	2	C82644	transcription regu
1129	67.5	4.8	690	2	D75487	v-type ATP synthas	1202	67	4.8	411	2	S61245	probable virion gl
1130	67.5	4.8	699	2	T12169	NADH2 dehydrogenas	1203	67	4.8	416	2	JN0720	glucosyl transfera
1131	67.5	4.8	703	2	T13074	NADH2 dehydrogenas	1204	67	4.8	417	2	AF3708	hypothetical prote
1132	67.5	4.8	741	2	T13404	NADH2 dehydrogenas	1205	67	4.8	421	2	AF2382	hypothetical prote
1133	67.5	4.8	741	2	T13760	NADH2 dehydrogenas	1206	67	4.8	423	2	S74031	conserved hypotet
1134	67.5	4.8	741	2	T13776	NADH2 dehydrogenas	1207	67	4.8	430	2	S74039	hypothetical prote
1135	67.5	4.8	741	2	T12762	NADH2 dehydrogenas	1208	67	4.8	446	2	AC3349	protein translocas
1136	67.5	4.8	744	2	T12694	NADH2 dehydrogenas	1209	67	4.8	453	2	A43765	stsl+ protein - fl
1137	67.5	4.8	744	2	T12611	NADH2 dehydrogenas	1210	67	4.8	453	2	T30985	hypothetical prote
1138	67.5	4.8	801	2	A89862	Na+/H+ antiporter	1211	67	4.8	456	2	A12789	manganese transpor
1139	67.5	4.8	812	2	T19446	hypothetical prote	1212	67	4.8	458	2	H71657	NADH2 dehydrogenas
1140	67.5	4.8	820	2	G82168	trimethylamine-N-O	1213	67	4.8	459	1	DNHUNA	NADH2 dehydrogenas
1141	67.5	4.8	823	2	S44873	ZC21.2 protein - C	1214	67	4.8	461	2	H97568	manganese transpor
1142	67.5	4.8	823	2	B81282	probable integral	1215	67	4.8	462	2	T34365	hypothetical prote
1143	67.5	4.8	890	2	H69877	calcium-transporti	1216	67	4.8	468	2	AD0521	probable symporter
1144	67.5	4.8	900	2	D97351	sensor protein Kdp	1217	67	4.8	469	2	T35670	hypothetical prote
1145	67.5	4.8	936	2	B64567	cytochrome c bioge	1218	67	4.8	470	2	T26602	hypothetical prote
1146	67.5	4.8	952	2	T32836	hypothetical prote	1219	67	4.8	473	2	AG0612	probable transpor
1147	67.5	4.8	1199	1	S76549	transcription-repa	1220	67	4.8	477	2	S71323	alpha-1A adrenergi
1148	67.5	4.8	1247	1	VHWN2	structural polypro	1221	67	4.8	485	2	C70488	cytochrome-c oxida
1149	67.5	4.8	1517	1	F65112	glutamate synthase	1222	67	4.8	491	2	G69251	proline permease (
1150	67.5	4.8	1517	2	F85985	glutamate synthase	1223	67	4.8	494	2	AC0133	probable permease
1151	67.5	4.8	1517	2	C91140	glutamate synthase	1224	67	4.8	511	2	H90439	hypothetical prote
1152	67.5	4.8	1704	2	T42749	ATP-binding casset	1225	67	4.8	516	2	T33269	hypothetical prote
1153	67.5	4.8	1767	2	S60124	transport protein	1226	67	4.8	517	2	AC2070	Na+/H+ antiporter
1154	67.5	4.8	1778	2	AF1116	internalin protein	1227	67	4.8	517	2	E82147	hypothetical prote
1155	67.5	4.8	2701	2	S17796	inositol-trisphosp	1228	67	4.8	522	2	F86215	protein T6D22.18 [
1156	67	4.8	90	2	E82861	conjugal transfer	1229	67	4.8	527	2	T49241	pectinesterase-lik
1157	67	4.8	109	2	C98018	crpB protein limpo	1230	67	4.8	537	2	D70478	conserved hypotet
1158	67	4.8	168	2	A72226	conserved hypotet	1231	67	4.8	546	2	AE0571	probable membrane
1159	67	4.8	180	2	C86290	hypothetical prote	1232	67	4.8	557	2	T46520	probable transmemb
1160	67	4.8	187	2	A95143	membrane protein [1233	67	4.8	557	2	S86888	probable transpor
1161	67	4.8	187	2	G98010	conserved hypotet	1234	67	4.8	557	2	G69096	hypothetical prote
1162	67	4.8	226	2	S57521	probable arsenical	1235	67	4.8	574	2	T41068	hypothetical prote
1163	67	4.8	232	1	G64591	conserved hypotet	1236	67	4.8	574	2	T34208	hypothetical prote
1164	67	4.8	259	2	S59152	cytochrome-c oxida	1237	67	4.8	584	2	B82810	ABC transporter ni
1165	67	4.8	260	2	A91138	hypothetical prote	1238	67	4.8	605	2	A36361	glucose transpor
1166	67	4.8	260	2	D65110	hypothetical 27.9	1239	67	4.8	625	2	T33792	hypothetical prote
1167	67	4.8	260	2	D85983	hypothetical prote	1240	67	4.8	625	2	AD2251	two-component sens
1168	67	4.8	261	2	T11826	cytochrome-c oxida	1241	67	4.8	640	2	D90174	hypothetical prote
1169	67	4.8	265	2	T05668	pollen allergen ho	1242	67	4.8	640	2	S44478	NADH2 dehydrogenas
1170	67	4.8	268	2	C86944	probable cation-ef	1243	67	4.8	653	2	T19245	hypothetical prote
1171	67	4.8	278	2	A93349	bacitracin resista	1244	67	4.8	659	2	C65022	yifg protein - Esc
1172	67	4.8	285	2	A84224	cytochrome c oxida	1245	67	4.8	698	2	T12586	NADH2 dehydrogenas
1173	67	4.8	287	2	B89936	hypothetical prote	1246	67	4.8	698	2	T12586	NADH2 dehydrogenas
1174	67	4.8	288	2	I78556	membrane glycoprot	1247	67	4.8	698	2	S76532	hypothetical prote
1175	67	4.8	291	2	S48977	glucose-1-phosphat	1248	67	4.8	699	2	T13778	NADH2 dehydrogenas
1176	67	4.8	293	2	D86065	glucose-1-phosphat	1249	67	4.8	707	2	G86894	hypothetical prote
1177	67	4.8	293	2	B91219	glucose-1-phosphat	1250	67	4.8	741	1	S34218	1,4-alpha-glucan b
1178	67	4.8	303	2	H65182	hypothetical prote	1251	67	4.8	741	2	T13764	NADH2 dehydrogenas
1179	67	4.8	308	2	H64409	hypothetical prote	1252	67	4.8	878	2	AD7385	TonB-dependent rec
1180	67	4.8	313	2	T24994	hypothetical prote	1253	67	4.8	918	2	A44257	interleukin-6 sign
1181	67	4.8	313	2	C95247	conserved hypotet	1254	67	4.8	970	2	F64230	spore germination
1182	67	4.8	313	2	H93111	conserved hypotet	1255	67	4.8	1001	2	T13807	potassium channel
1183	67	4.8	314	2	F81699	peptide ABC tranep	1256	67	4.8	1218	2	S38182	probable transpor
1184	67	4.8	323	2	AB0427	octaprenyl-diphosp	1257	67	4.8	1440	2	JC6312	protein-tyrosine-p
1185	67	4.8	328	2	D72566	hypothetical prote	1258	67	4.8	1457	1	A48066	protein-tyrosine-p
1186	67	4.8	349	2	AD0990	probable membrane	1259	67	4.8	1489	2	S73015	polyketide synthas
1187	67	4.8	354	2	C82038	nitrogen regulatio	1260	67	4.8	1559	2	A12348	ferredoxin-glutana
1188	67	4.8	356	2	B84749	hypothetical prote	1261	67	4.8	1758	2	F88559	protein C48B4.4b [
1189	67	4.8	364	2	T45253	probable antiporte	1262	67	4.8	2183	2	S47307	genome polypotein
1190	67	4.8	364	2	T24418	hypothetical prote	1263	66.5	4.8	175	2	A95058	conserved domain p
1191	67	4.8	367	2	D23349	hypothetical prote	1264	66.5	4.8	185	2	B97927	hypothetical prote
1192	67	4.8	371	2	D97790	octaprenyl-diphosp	1265	66.5	4.8	185	2	D81327	probable integral
1193	67	4.8	377	2	B71699	cell division prot	1266	66.5	4.8	205	2	A87460	Deda family protei
1194	67	4.8	388	2	B64459	Na+/H+-exchangin	1267	66.5	4.8	217	2	B69396	hypothetical prote
1195	67	4.8	394	2	AH0020	conserved integral	1268	66.5	4.8	245	2	F71887	hypothetical prote
1196	67	4.8	397	2	B70763	probable membrane	1269	66.5	4.8	256	2	G82804	phosphatidyltransf
1197	67	4.8	401	2	H82175	multidrug resistan	1270	66.5	4.8	258	2	A69830	hypothetical prote

1271	66.5	4.8	261	2	I64249	hypothetical prote	1344	66.5	4.8	744	2	T13063	NADH2 dehydrogenas
1272	66.5	4.8	269	2	A86889	zinc ABC transport	1345	66.5	4.8	744	2	T13048	NADH2 dehydrogenas
1273	66.5	4.8	279	2	E65226	hypothetical prote	1346	66.5	4.8	746	2	T01536	hypothetical prote
1274	66.5	4.8	292	2	A70546	probable menA prot	1347	66.5	4.8	755	2	T20950	hypothetical prote
1275	66.5	4.8	292	2	F83823	hypothetical prote	1348	66.5	4.8	759	2	D70422	cellulose synthase
1276	66.5	4.8	293	2	T41928	hypothetical prote	1349	66.5	4.8	790	2	G90477	hypothetical prote
1277	66.5	4.8	295	2	AE0993	glycerol-3-phospha	1350	66.5	4.8	812	2	T16621	hypothetical prote
1278	66.5	4.8	306	2	C70141	oligopeptide ABC t	1351	66.5	4.8	820	2	T41978	helicase - human h
1279	66.5	4.8	306	2	S55047	ABC-type transport	1352	66.5	4.8	860	2	C82750	mannosyltransferas
1280	66.5	4.8	320	2	T23635	hypothetical prote	1353	66.5	4.8	919	2	S19810	glutamate receptor
1281	66.5	4.8	361	2	T37938	hypothetical prote	1354	66.5	4.8	919	2	I53474	kainate receptor -
1282	66.5	4.8	366	2	G95376	conserved hypotet	1355	66.5	4.8	937	2	T137241	olfactory channel
1283	66.5	4.8	375	2	T05707	phosphate transport	1356	66.5	4.8	957	2	D86651	protein B0212.5 [i
1284	66.5	4.8	385	2	B87441	rod shape-determin	1357	66.5	4.8	999	2	T27628	hypothetical prote
1285	66.5	4.8	389	2	AD1378	cell division prot	1358	66.5	4.8	1002	2	G97217	conserved membrane
1286	66.5	4.8	390	2	AH0260	conserved hypotet	1359	66.5	4.8	1010	1	PXZP2P	H+-exporting ATPas
1287	66.5	4.8	394	2	T13721	NADH2 dehydrogenas	1360	66.5	4.8	1049	2	T22762	hypothetical prote
1288	66.5	4.8	405	2	T40193	hypothetical prote	1361	66.5	4.8	1068	2	AB1082	B' subtilis YueB p
1289	66.5	4.8	409	2	B85735	probable membrane	1362	66.5	4.8	1088	2	H84604	probable cellulose
1290	66.5	4.8	410	2	E75290	probable multidrug	1363	66.5	4.8	1248	2	C89874	autolysin [limpor
1291	66.5	4.8	411	2	S73218	preprotein translo	1364	66.5	4.8	1704	2	S71363	probable ATP-bindi
1292	66.5	4.8	421	2	E90883	hypothetical prote	1365	66.5	4.8	1704	2	A59188	ATP-binding casset
1293	66.5	4.8	422	2	H69839	multidrug resistan	1366	66	4.7	101	2	G69894	hypothetical prote
1294	66.5	4.8	428	2	G82918	hypothetical prote	1367	66	4.7	105	2	AH2209	hypothetical prote
1295	66.5	4.8	438	2	H91112	hypothetical prote	1368	66	4.7	158	2	S58016	probable olfactory
1296	66.5	4.8	438	2	H85957	partial probable t	1369	66	4.7	171	2	S44146	amiS protein - Pse
1297	66.5	4.8	440	2	T13863	probable aminotran	1370	66	4.7	172	2	A83226	hypothetical prote
1298	66.5	4.8	441	2	T19306	hypothetical prote	1371	66	4.7	195	1	CYHYAM	alpha-crystallin c
1299	66.5	4.8	452	2	D68635	maltose ABC transp	1372	66	4.7	196	2	AD2304	hypothetical prote
1300	66.5	4.8	454	2	A70079	conserved hypotet	1373	66	4.7	203	2	T05519	hypothetical prote
1301	66.5	4.8	467	2	F90544	conserved hypotet	1374	66	4.7	203	2	C85288	hypothetical prote
1302	66.5	4.8	467	2	T16319	hypothetical prote	1375	66	4.7	204	2	D89097	hypothetical prote
1303	66.5	4.8	469	2	H70626	probable narX3 pro	1376	66	4.7	211	2	E89963	hypothetical prote
1304	66.5	4.8	471	2	F71543	probable dicarboxy	1377	66	4.7	255	2	AH0577	molycopsterin-cont
1305	66.5	4.8	472	2	E83497	probable amino aci	1378	66	4.7	256	2	J01106	tonoplast intrinsi
1306	66.5	4.8	474	2	S07754	NADH2 dehydrogenas	1379	66	4.7	260	2	AG0904	probable membrane
1307	66.5	4.8	475	2	T46745	arginine/ornithine	1380	66	4.7	265	2	H90254	sulfate ABC transp
1308	66.5	4.8	478	2	D64895	probable membrane	1381	66	4.7	267	2	A87233	conserved membrane
1309	66.5	4.8	480	2	D90038	PTS system, sucros	1382	66	4.7	275	2	F83222	Na+ protein PA339
1310	66.5	4.8	484	2	E75138	osmoregulated prol	1383	66	4.7	276	2	B35252	hema concentration
1311	66.5	4.8	491	2	H84379	4-hydroxybutyrate	1384	66	4.7	280	2	F75057	hypothetical prote
1312	66.5	4.8	492	2	T15603	hypothetical prote	1385	66	4.7	285	2	E84789	hypothetical prote
1313	66.5	4.8	498	2	AI0482	phosphate transport	1386	66	4.7	285	2	D84789	hypothetical prote
1314	66.5	4.8	499	2	A65085	probable low-affin	1387	66	4.7	285	2	S44085	plasma membrane in
1315	66.5	4.8	509	2	T11043	cytochrome-c oxida	1388	66	4.7	296	2	G72760	hypothetical prote
1316	66.5	4.8	513	2	T14864	probable monosacch	1389	66	4.7	298	2	T13684	NADH2 dehydrogenas
1317	66.5	4.8	513	2	C81859	probable integral	1390	66	4.7	303	2	AB1772	cation transport p
1318	66.5	4.8	519	2	E90548	conserved hypotet	1391	66	4.7	307	2	T16457	hypothetical prote
1319	66.5	4.8	520	2	D90014	hypothetical prote	1392	66	4.7	311	2	AI2697	permease [imported
1320	66.5	4.8	526	2	H85891	hydrogenase 4 memb	1393	66	4.7	311	2	B97480	hypothetical prote
1321	66.5	4.8	526	2	E65024	Hydrogenase-4 comp	1394	66	4.7	312	2	G69423	branched-chain ami
1322	66.5	4.8	530	2	T11284	cytochrome-c oxida	1395	66	4.7	312	2	H90517	hypothetical prote
1323	66.5	4.8	553	2	T38541	probable sucrose c	1396	66	4.7	318	2	AI1811	hypothetical prote
1324	66.5	4.8	557	2	T49811	probable vacuolar	1397	66	4.7	320	2	T25308	hypothetical prote
1325	66.5	4.8	569	2	T33706	probable sodium/hy	1398	66	4.7	322	2	T13486	NADH2 dehydrogenas
1326	66.5	4.8	573	2	T23102	hypothetical prote	1399	66	4.7	330	1	H69798	conserved hypotet
1327	66.5	4.8	574	2	G84578	probable potassium	1400	66	4.7	335	2	T39425	hypothetical prote
1328	66.5	4.8	648	2	C97961	DNA topoisomerase	1401	66	4.7	336	2	T31762	hypothetical prote
1329	66.5	4.8	648	2	F95093	DNA gyrase chain B	1402	66	4.7	344	2	AB3236	hypothetical prote
1330	66.5	4.8	649	2	AB2154	hypothetical prote	1403	66	4.7	354	2	S70595	NADH2 dehydrogenas
1331	66.5	4.8	659	2	S67175	probable membrane	1404	66	4.7	355	2	A64138	rfe protein - Haem
1332	66.5	4.8	660	1	S54746	cytochrome c-type	1405	66	4.7	357	2	T03557	ribose transport s
1333	66.5	4.8	664	2	B53610	ntpf protein - Ent	1406	66	4.7	357	2	F81916	probable integral
1334	66.5	4.8	679	2	H95036	glycosyl hydrolase	1407	66	4.7	371	2	AD1201	N-acyl-L-amino aci
1335	66.5	4.8	699	2	T12173	NADH2 dehydrogenas	1408	66	4.7	377	2	H64387	hypothetical prote
1336	66.5	4.8	703	2	H86588	thio-disulfide int	1409	66	4.7	381	2	C71680	hypothetical prote
1337	66.5	4.8	703	2	H72034	thiol-disulfide in	1410	66	4.7	383	2	E87680	hypothetical prote
1338	66.5	4.8	714	2	G81503	thiol-disulfide in	1411	66	4.7	395	2	A86527	neutral amino acid
1339	66.5	4.8	725	2	S25990	phenylalanine ammo	1412	66	4.7	395	2	E72095	neutral amino acid
1340	66.5	4.8	732	2	AD0014	primosomal protein	1413	66	4.7	396	2	AH2859	MFS permease [limpo
1341	66.5	4.8	737	2	D97907	alpha-xylosidase (1414	66	4.7	396	2	F97636	probable transport
1342	66.5	4.8	741	2	T12605	NADH2 dehydrogenas	1415	66	4.7	398	2	H75043	mg2+ transport pro
1343	66.5	4.8	741	2	T13361	NADH2 dehydrogenas	1416	66	4.7	404	2	S65991	membrane protein y

Db 848 FAIAAMVWALIRNIPGLEVLVLSRLNNROGASYAITILNVIIVAGMVTFGSLGV 907
QY 103 -----CLGISVANFQKTLFAAHVSGAVLTF-----GMGSLYMF 137
Db 908 SMDKLQWLAAALSVGLGLOEFGVSGVGLIILFERPVRIGDVTVIGTYSGTVKIRIR 967
QY 138 VOTILSYQMPKIHGQVFWIRLLLVIMCGVSALSMLTCSVLSHG-NFGTDLQKHLWN 196
Db 968 ATTITDFRKEVIIPNKAFT-VERLINW-----SLSDTTTLRLVIRLGVAVGSDLEK----- 1017
QY 197 PEDKGVVLMHMTAA-----EWSMSFSFPGF-----PLTVIRDFQKLSRVE 238
Db 1018 -----VKRVLLOAAMEHPKVMHDEPAVFFTFGASTLDHRLRYRELDRSHTV 1069

RESULT 6
E72523
carbon starvation protein A homolog APE2162 [similarity] - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E72523
R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yanazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-604 <NAW>
A:Cross-references: UNIPROT:Q9Y9X7; UNIPARC:UPI000005E231; DDBJ:AF000063; NID:G5105654;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2162
C:Superfamily: carbon starvation protein

Query Match 7.0%; Score 97; DB 2; Length 604;
Best Local Similarity 23.9%; Pred. No. 1.1;
Matches 69; Conservative 39; Mismatches 101; Indels 80; Gaps 16;

QY 4 FQOGLSFLPSAL--VWTSAAIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGMLN 61
Db 183 YRMGLMGSPSTVITVLVIAAFVYSYNHGIVIGTFDPSLP-FOEGGWAYHRWVI--ILG 239
QY 62 IAAVLICATIVRYKQVHVSPEENVIIKLNKAGLVGLILGILSGLSVANFQKTLFAAH 121
Db 240 LVALLA-ASLPWY-----LLQPRD-----YLNAYILWTG-----LGLAAIA---AILLGTQS 283
QY 122 VSGAVLTFMGSLYMFVQVITLSYQMPKIHGQVFWIRLLLVIMCGVSALSMLTCSVLSH 181
Db 284 LKGPAYT-----SFQPNIIAGQPTP-----FWPAIPLIACG-----SLSGFHSLSVA 325
QY 182 SGNFGTDLEQKLN-----WV-PE--DKGYV-LHMITTA 210
Db 326 SGTTSKQLASELDALFPVGYGAMLLLEGALSGLAVIIPISPAWNAPELIQKGVIEENMLDLA 385
QY 211 A-----EWSMSFSFPGFPLTVIRDFQKLSRVEANLHGLTYLD 249
Db 386 AVPRYAVGYTLAKTFEMFGVGTGYSFFTFLFASLMUSMYLTLTLD 434

RESULT 7
S43882
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - garden lettuce mitochondrion
C:Species: Mitochondrion Lactuca sativa (garden lettuce)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S43882
R:Geiss, K.T.; Abbas, G.M.; Makaroff, C.A.
Mol. Gen. Genet. 243, 97-105, 1994
A:Title: Intron loss from the NADH dehydrogenase subunit 4 gene of lettuce mitochondrion
A:Reference number: S43882; MUID:94247363; PMID:8190077
A:Accession: S43882

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-495 <GEI>
A:Cross-references: UNIPROT:Q37544; UNIPARC:UPI000008E589
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.9%; Score 96; DB 2; Length 495;
Best Local Similarity 24.6%; Pred. No. 1.1;
Matches 55; Conservative 34; Mismatches 83; Indels 52; Gaps 12;

QY 8 LSFLPSALVWTSAAIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAM--LNI----- 62
Db 277 LCFTF---FIYTLSAIAIIYTSLLTLRQID--LKKIIAYSSVAHMLNLTIGMPSLNIQGI 331
QY 63 -----AAVLICATIVRYKQ-----VHALSPEENVIIKLNKAGLV 98
Db 332 GGSILLMLSHGLVSSALFLCVGLVYRHKTRLVRYGGLVSTMPNPSTIFFFTLANMSL 391
QY 99 -GILSCLG--LSIVANFQKTLFAAHVSGAVLTFMGSLYMFVQVITLSYQMP----- 148
Db 392 PGTSTFIFGEFLTLVGAFQNSLVATLALGMILGAAYSLWLY-NRVVSGNLKPPDFLHKFS 450
QY 149 KIHGQVFWIRLLLVIMCGVSALSMLTCT-----SSVLHSGNF 185
Db 451 DLNKGTEVFIFPLVGVVMGVYKVPFPCMHTSVSNLVQHGKF 494

RESULT 8
S16447
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - wheat mitochondrion
N:Alternate names: mitochondrial complex I subunit IV
C:Species: Mitochondrion Triticum aestivum (common wheat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S16447; S16448; S06835
R:Ramattina, L.; Grienemberger, J.M.
Nucleic Acids Res. 19, 3275-3282, 1991
A:Title: RNA editing of the transcript coding for subunit 4 of NADH dehydrogenase in wh
A:Reference number: S16447; MUID:91288205; PMID:1712098
A:Accession: S16447
A:Molecule type: mRNA
A:Residues: 1-495 <LAW>
A:Cross-references: UNIPROT:P27572; UNIPARC:UPI00001720FA; EMBL:X57163
A:Note: the authors translated the codon CGT for residue 418 as Ala
A:Accession: S16448
A:Molecule type: DNA
A:Residues: 1-14, 'P', 16-24, 'TP', 27-35, 'P', 37-51, 'PP', 54, 'PR', 57-65, 'S', 67-105, 'S', 107-1
'H', 474-477, 'P', 479-495 <LAF>
A:Cross-references: UNIPARC:UPI000013079C; EMBL:X57164; NID:G21823; PIDN:CAA40453.1; PI
A:Note: the authors translated the codon CGT for residue 418 as Ala
A:Note: 15-P, 25-Thr, 26-Pro, 36-Pro, 52-Pro, 53-Pro, 55-Pro, 56-Arg, 66-Ser, 106-Ser, 1
re due to RNA editing
R:Ramattina, L.; Weil, J.H.; Grienemberger, J.M.
FEBS Lett. 258, 79-83, 1989
A:Title: RNA editing at a splicing site of NADH dehydrogenase subunit IV gene transcrip
A:Reference number: S06835; MUID:90076495; PMID:2687023
A:Accession: S06835
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 295-346 <LAW>
A:Cross-references: UNIPARC:UPI00001720FB
C:Genetics:
A:Gene: nad4
A:Genome: mitochondrion
A:Introns: 154/2; 326/1; 467/1
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.8%; Score 94; DB 1; Length 495;
Best Local Similarity 24.1%; Pred. No. 1.7;
Matches 54; Conservative 34; Mismatches 84; Indels 52; Gaps 11;

QY 8 LSFLPSALVWTSAAIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAM--LNI----- 62

Db 277 LCFTP---PIYLSAIIYTSITLRLQID--LKIIAYSSVAHWNVLTVIGFNSLNIQGI 331
QY 63 -----AAVLCIATIVRYKQ-----VHALSPEENVIIKLNKAGLVL 98
Db 332 GGSILLMLSHGLVSSALFLQCVGLVDRHKTRLVRYVGGVLTWPNFSTFFFTLANMSL 391
QY 99 -GILSCLG--LSIVANFQKTLTFAAHVSGAVLTFMGSLYMFVQITLSYQOMP----- 148
Db 392 PGTSSFIGBFLILVGAFOFNSIVATLRALGMILGAAYSLWLY-NRVVSGNLKPDFLYKFS 450
QY 149 KTHGKQVFWIR--LLLVICWGVSAISMLTCTC-----SSVLHSGNF 185
Db 451 DINGREVFIFLFLVGVVGMGVYKPVFLDCMTSVSNLVQHGKF 494

RESULT 9
D96506
hypothetical protein T12C22.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D96506
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96506
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <STO>
A:Cross-references: UNIPROT:Q9LPP6; UNIPARC:UPI000000BFD0; GB:AE005173; NID:g8655985; P
C:Genetics:
A:Map position: 1
C:Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70

Query Match 6.7%; Score 93.5; DB 2; Length 379;
Best Local Similarity 21.8%; Pred. No. 1.4;
Matches 47; Conservative 53; Mismatches 95; Indels 21; Gaps 9;
QY 10 FLPSALVIVTSAAFIPSYITAVTLHHIDPALPYISDTGTVAPEKCLFG-AMLNIAA--- 64
Db 90 YIP--LLLLPSSASVESSESSCLXYI--VLIVLGVIIAGDNMLYSVGLLYLSASTYS 145
QY 65 VLICIATIVRYKQVHALSPEENVIIKLNKAGLVGLSCLGSLSIIVANFQKTLTFAAHVSG 124
Db 146 LICATQAPNAVFSYFIPNAQKFTALILNSVLLSPSAALIALNDADTSGVSRSKYIVG 205
QY 125 AVLTFGMGSLYMFVQITLSYQOMPKHGKQVFWIRLLLVICWGVSAISMLTCTCSSLVHSGN 184
Db 206 FVCTLAASALYSLLSLMLQFSPE-KILKRETFSVLEMQIYTSLVA---TCVSVI--GL 258
QY 185 FGTDLQKLHNPE--DKG---YVLHMITTAAEWSM 215
Db 259 PASGEWRTLHGEVGHKQASVLTLVWTVATWQV 294

RESULT 10
F71651
putrescine-ornithine antiporter (potE) RP483 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 05-Oct-2004
C:Accession: F71651
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: F71651
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-429 <AND>
A:Cross-references: UNIPROT:Q9ZD63; UNIPARC:UPI00000D37BE; GB:AJ235272; GB:AJ235269; NFI
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: potE, RP483
C:Superfamily: ecotropic retrovirus receptor protein

Query Match 6.7%; Score 93.5; DB 2; Length 429;
Best Local Similarity 24.1%; Pred. No. 1.6;
Matches 48; Conservative 37; Mismatches 79; Indels 35; Gaps 10;
QY 11 LPSALVIVTSAAFIPSYITAVTLHHIDPA-----LPYISDTGTVAPEKCLFGAMLN-- 61
Db 217 IPRAIIIGTCCVAPLYIINSIGIIPASELINSKAPY-ADAATL-----LFGGTWSKV 270
QY 62 ---TAAVLCIATI---YVRYKQVHALSPEENVIIKL-----NKAGLVGLSCLGSLTIV 109
Db 271 ITVIASVTCIGTLNAAVLTSQGIALLGLAEDGLLPKFFAKNSNNAPTYGIIISLCIGITPL 330
QY 110 ANFQKTTLFAAHVSGAVLTFMGSLYMFVQITLSYQOMPKI-HGKQVFWIRLLLVICWGV 168
Db 331 LLFTSNNAFAQIIT-QIIDFSV-TAFLFVLYLCSLAFLKVFSSKENFSYYVLF-----V 383
QY 169 SALSMLTCTCSSVLHSGNFCT 187
Db 384 AIISIFCTWVIYKTPFET 402

RESULT 11
F90693
mechanosensitive channel protein [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F90693
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90693
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1120 <HAY>
A:Cross-references: UNIPROT:Q8XD54; UNIPARC:UPI00000D03CB; GB:BA000007; PIDN:BA833941.1;
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: EC90518

Query Match 6.7%; Score 93; DB 2; Length 1120;
Best Local Similarity 19.6%; Pred. No. 5;
Matches 46; Conservative 38; Mismatches 85; Indels 66; Gaps 8;
QY 1 MWFOQGLSFLPSALVIVTSAAFIPSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 805 MFW-----AIWSDLIITVPSYILSDISITLWHYNG-----TEAGAAVVKXNVMTGSL 847
QY 61 -----NIAVLCIATIVRYKQVHALSPEENVIIKLNKAGLVGLS- 102
Db 848 FAIIASVNAVAILRNLPGILLEVLVLSRLNMKGASVYAITILNYIIIAVGAMTVFGLGV 907
QY 103 -----CLGLSIVANFQKTLTFAAHVSGAVLTF-----GMGSLYMF 137
Db 908 SWDKLQWLAAALSVGLGFLQEIFGNFVSGLLILPERPVRIGDVTVTIGSFSGTSVKIRIR 967
QY 138 VQITLSYQOMPKHGKQVFWIRLLLVICWGVSAISMLTCTCSSVLHSG-NFGTDLEQ 191
Db 968 ATTITDFRKEVFIIPNKAF-VTERLINW----SLTDTTTLRLVIRLGVAYGSDLEK 1017

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 7, 2006, 16:27:57 ; Search time 247 Seconds
(without alignments)
759.800 Million cell updates/sec

Title: US-1b-006-867-2
Perfect score: 1392
Sequence: 1 MMWFOGLSFLPSALVITMS.....YDTAPCPINNERTLLSRDI 266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1392	100.0	266	2	Q6UX65 HUMAN
2	1383	99.4	266	2	Q4VMF6 HUMAN
3	1245	89.4	267	2	Q9CR48 MOUSE
4	1236	88.8	267	2	Q5BK09 RAT
5	1235	88.7	267	2	Q9D520 MOUSE
6	805.5	57.9	180	2	Q9D835 MOUSE
7	764.5	54.9	272	2	Q61Q10 BRARE
8	725	52.1	136	2	Q8NB04 HUMAN
9	492.5	35.4	238	2	Q8N682 HUMAN
10	479.5	34.4	238	2	Q9DC58 MOUSE
11	477.5	34.3	240	2	Q5XUL0 BRARE
12	476.5	34.2	240	2	Q5RGJ7 BRARE
13	473.5	34.0	239	2	Q5SAK8 XENTR
14	471.5	33.9	287	2	Q6NRS6 XENLA
15	439.5	31.6	238	2	Q8QGB2 ONCMY
16	388.5	27.9	237	2	Q7QE61 ANOGA
17	361.5	26.0	246	2	Q77262 DROME
18	332.5	23.9	267	2	Q5DAX3 SCHJA
19	318.5	22.9	252	2	Q86F93 SCHJA
20	288	20.7	271	2	Q93319 CAEL
21	277	19.9	73	2	Q4T6B8 TETNG
22	267.5	19.2	231	2	Q4V7T3 XENLA
23	262	18.8	238	2	Q8R218 MOUSE
24	260	18.7	293	2	Q61P61 CAEBR
25	258.5	18.6	230	2	Q4V7T7 XENLA
26	251.5	18.1	181	2	Q6XHF5 DROYA
27	251	18.0	132	2	Q9NUN1 HUMAN
28	248	17.8	257	2	Q5DGL6 SCHJA
29	247	17.7	132	2	Q5EA39 BOVIN
30	240	17.2	132	2	Q78J26 MOUSE
31	203	14.6	249	2	Q8C8S3 MOUSE

32	201.5	14.5	271	2	Q6GPL4 XENLA
33	191.5	13.8	257	2	Q61QJ3 BRARE
34	188.5	13.5	308	2	Q4SA40 TETNG
35	185.5	13.3	219	2	Q696P1 MOUSE
36	183.5	13.2	294	2	Q78KK4 BRARE
37	174.5	12.5	243	2	Q559G4 DICDI
38	172.5	12.4	243	2	Q861K0 DICDI
39	161.5	11.6	123	2	Q8C9L9 MOUSE
40	160.5	11.5	271	2	Q86TGI HUMAN
41	157.5	11.3	271	2	Q9QZE9 RAT
42	153.5	11.0	760	2	Q4SKZ5 TETNG
43	151.5	10.9	271	2	Q91WN2 MOUSE
44	150.5	10.8	243	2	Q86K17 DICDI
45	147.5	10.6	251	2	Q556P1 DICDI
46	133.5	9.6	233	2	Q4T6B7 TETNG
47	120.5	8.7	207	2	Q550K4 DICDI
48	120	8.6	224	2	Q23135 CAEL
49	119.5	8.6	273	2	Q628C5 CAEBR
50	117.5	8.4	246	2	Q61U88 CAEBR
51	112.5	8.1	252	2	Q9U3J7 CAEL
52	107.5	7.7	435	2	Q7QJU9 ANOGA
53	106.5	7.7	140	2	Q8K117 MOUSE
54	105.5	7.6	207	2	Q54KE7 DICDI
55	105.5	7.6	881	2	Q5HAJ2 EHRRW
56	105	7.5	217	2	Q5NE86 FRATT
57	103	7.4	299	2	Q6CDS5 VARLI
58	103	7.4	332	1	HMSC ARCTU
59	103	7.4	643	2	Q5SR58 CRYNE
60	103	7.4	643	2	Q5KG81 CRYNE
61	101.5	7.3	255	2	Q9VPT7 DROME
62	101.5	7.3	332	2	Q650W2 ORYZA
63	101.5	7.3	881	2	Q5FG25 EHRRG
64	101	7.3	218	2	Q8N2R6 HUMAN
65	101	7.3	293	2	Q6SRP9 MANSM
66	101	7.3	495	1	NUAM ARATH
67	101	7.3	539	2	Q8EJE2 SHEON
68	98.5	7.1	456	2	Q6D428 ERWCT
69	98.5	7.1	1120	2	Q5PFL4 SALPA
70	98.5	7.1	1120	2	Q828T6 SALTI
71	98.5	7.1	1120	2	Q8ZRA5 SALT
72	98.5	7.1	1140	2	Q57S86 SALCH
73	98	7.0	495	2	Q6YSN0 BRANA
74	98	7.0	664	2	Q8M8A9 BETVU
75	97.5	7.0	664	2	Q666D8 CAEL
76	97.5	7.0	746	2	Q9N5Q3 CAEL
77	97	7.0	390	2	Q8XQMO RALSO
78	97	7.0	604	2	Q9Y9X7 AERPE
79	96.5	6.9	608	2	Q4HX42 GIBZE
80	96	6.9	395	2	Q8EFB8 SHEON
81	96	6.9	495	2	Q37544 LACSA
82	96	6.9	615	2	Q7SLC5 NEUCR
83	95.5	6.9	268	2	Q5WSU3 LEGPL
84	95.5	6.9	284	2	Q4ZM21 PSESY
85	95.5	6.9	291	2	Q9ZFP3 ENTFC
86	95.5	6.9	309	2	Q6NRD6 XENLA
87	95.5	6.9	388	2	Q4PKD8 USTMA
88	95.5	6.9	486	2	Q8FPF5 COREP
89	95	6.8	440	2	Q4WU03 ASPFU
90	95	6.8	702	2	Q9SC10 WMAGN
91	94.5	6.8	229	2	Q4RR14 TETNG
92	94.5	6.8	268	2	Q5X117 LEGPA
93	94.5	6.8	469	2	Q7UF66 RUOBA
94	94.5	6.8	724	2	Q6FU10 CANGA
95	94	6.8	266	2	Q4FWG7 LEIMA
96	94	6.8	283	2	Q8SMV8 PSEPK
97	94	6.8	452	2	Q5F109 LACAC
98	94	6.8	495	1	NU4M WHEAT
99	94	6.8	820	2	Q61KL4 CAEBR
100	94	6.8	1120	2	Q8FK90 ECOL6
101	93.5	6.7	379	2	Q9LPF6 ARATH
102	93.5	6.7	429	2	Q9ZD63 RICPR
103	93.5	6.7	440	2	Q4QMF2 HAEI8
104	93.5	6.7	1624	2	Q4I335 GIBZE

Q6GPL4	xenopus lae
Q61QJ3	brachydanio
Q4SA40	tetraodon n
Q696P1	mus musculus
Q78KK4	brachydanio
Q559G4	dictyosteli
Q861K0	dictyosteli
Q8C9L9	mus musculus
Q86TGI	homo sapien
Q9QZE9	rattus norv
Q4SKZ5	tetraodon n
Q91WN2	mus musculus
Q86K17	dictyosteli
Q556P1	dictyosteli
Q4T6B7	tetraodon n
Q550K4	dictyosteli
Q23135	caenorhabdi
Q628C5	caenorhabdi
Q61U88	caenorhabdi
Q9U3J7	caenorhabdi
Q7QJU9	anopheles g
Q8K117	mus musculus
Q54KE7	dictyosteli
Q5HAJ2	ehrllichia r
Q5NE86	francisella
Q6CDS5	yarrowia li
Q29749	archaeoglob
Q5SR58	cryptococcu
Q5KG81	cryptococcu
Q9VPT7	drosofila
Q650W2	oryza sativ
Q5FG25	ehrllichia r
Q8N2R6	homo sapien
Q6SRP9	mannheimia
P93133	arabidopsis
Q8EJE2	shewanella
Q6D428	erwinia car
Q5PFL4	salmonella
Q828T6	salmonella
Q8ZRA5	salmonella
Q57S86	salmonella
Q6YSN0	brassica na
Q8M8A9	beta vulgar
Q666D8	caenorhabdi
Q9N5Q3	caenorhabdi
Q8XQMO	raletonia s
Q9Y9X7	aeropyrum p
Q4HX42	gibberella
Q8EFB8	shewanella
Q37544	lactuca sat
Q7SLC5	neurospora
Q5WSU3	legionella
Q4ZM21	pseudomonas
Q9ZFP3	enterococcu
Q6NRD6	xenopus lae
Q4PKD8	ustilago ma
Q8FPF5	corynebacte
Q4WU03	aspergillus
Q9SC10	tetracera a
Q4RR14	tetraodon n
Q5X117	legionella
Q7UF66	rhodospirell
Q6FU10	candida gla
Q4FWG7	leishmania
Q8SMV8	pseudomonas
Q5F109	lactobacill
P27572	tritricum ae
Q61KL4	caenorhabdi
Q8FK90	escherichia
Q9LPF6	arabidopsis
Q9ZD63	rickettsia
Q4QMF2	haemophilus
Q4I335	gibberella

105	93	6.7	576	2	Q52SX8_LEGPH	Q52sx8	legionella	178	89	6.4	659	2	Q7VUV3_BORPE	Q7vuv3	bordetella
106	93	6.7	797	2	Q45585_CABEL	Q45585	caenorhabdi	179	89	6.4	660	2	Q7WBD6_BORPA	Q7wbd6	bordetella
107	93	6.7	1120	1	KEFA_ECOLI	P77338	escherichia	180	89	6.4	757	2	Q9UF82_HUMAN	Q9ufa2	homo sapien
108	93	6.7	1120	2	Q83SE8_SHIFL	Q83se8	shigella fl	181	89	6.4	917	2	Q9H698_HUMAN	Q9h698	homo sapien
109	93	6.7	1120	2	Q8XD54_ECO57	Q8xd54	escherichia	182	89	6.4	1011	2	Q96F81_HUMAN	Q96f81	homo sapien
110	93	6.7	1264	2	Q6BT03_DEBHA	Q6bt03	debaromyce	183	88.5	6.4	266	2	Q4IXM4_AZOVI	Q4ixm4	azotobacter
111	92.5	6.6	251	2	Q970A1_SULTO	Q970a1	sulfolobus	184	88.5	6.4	361	1	MRAY_COXBU	Q83f26	coxiella bu
112	92.5	6.6	473	2	Q82506_SALTI	Q82506	salmonella	185	88.5	6.4	361	1	MRAY_LEGPA	Q5x183	legionella
113	92.5	6.6	473	2	Q8ZNC5_SALTY	Q8znc5	salmonella	186	88.5	6.4	403	2	Q5SXU0_CRYNE	Q5sxu0	cryptococcus
114	92.5	6.6	479	2	Q6SGM5_9BACT	Q6sgm5	uncultured	187	88.5	6.4	403	2	Q5KM52_CRYNE	Q5km52	cryptococcus
115	92.5	6.6	634	2	Q5KSP7_9ECHI	Q5ksp7	astropecten	188	88.5	6.4	430	2	Q9V210_PYRAB	Q9v210	pyrococcus
116	92.5	6.6	977	2	Q6CX54_KLUFLA	Q6cx54	kluveromyc	189	88.5	6.4	680	2	Q5SBY7_9ASTE	Q5sby7	vahlia cape
117	92.5	6.6	1117	2	Q4KJF2_PSEFS	Q4kfj2	pseudomonas	190	88.5	6.4	691	2	Q8M8V0_9ASTE	Q8m8v0	vahlia cape
118	92	6.6	434	2	Q7VN68_HAEDU	Q7vn68	haemophilus	191	88.5	6.4	732	2	Q9TJF3_9GENT	Q9tjf3	sinira viri
119	92	6.6	454	2	Q513Q7_ENTHI	Q513q7	entamoeba h	192	88.5	6.4	732	2	Q9TUS2_9GENT	Q9tus2	pentagonia
120	92	6.6	594	2	Q5V2N6_HALMA	Q5v2n6	haloarcula	193	88.5	6.4	807	2	Q5CZ47_CAEEL	Q5cz47	caenorhabdi
121	91.5	6.6	268	2	Q5ZRL1_LEGPH	Q5zrl1	legionella	194	88.5	6.4	808	2	Q21453_CAEEL	Q21453	caenorhabdi
122	91.5	6.6	387	2	Q22188_CAEEL	Q22188	caenorhabdi	195	88.5	6.4	833	2	Q7USM4_RHOBA	Q7usm4	rhodopirell
123	91.5	6.6	430	2	Q810LA_CAEEL	Q810la	caenorhabdi	196	88	6.3	290	2	Q4MVA6_BACCE	Q4mva6	bacillus ce
124	91.5	6.6	444	2	Q67EN8_CALSI	Q67en8	callinectes	197	88	6.3	290	2	Q6HC79_BACHK	Q6hc79	bacillus th
125	91.5	6.6	447	2	Q5QZ24_IDILO	Q5qz24	idiomarina	198	88	6.3	290	2	Q632P0_BACCC	Q632p0	bacillus th
126	91.5	6.6	477	2	Q5U6C1_BETVU	Q5u6c1	beta vulgar	199	88	6.3	290	2	Q81KE4_BACAN	Q81ke4	bacillus an
127	91.5	6.6	495	2	Q9MF62_BETVU	Q9mf62	beta vulgar	200	88	6.3	324	2	Q4SF91_TETNG	Q4sf91	tetraodon n
128	91.5	6.6	530	2	Q8W48_LACPL	Q8w48	lactobacill	201	88	6.3	372	2	Q8A1P0_BACTN	Q8a1p0	bacteroides
129	91.5	6.6	712	1	POTL_ARATH	Q22397	arabidopsis	202	88	6.3	413	2	Q8R792_THETN	Q8r792	thermoanaer
130	91.5	6.6	712	2	Q56YD6_ARATH	Q56yde	arabidopsis	203	88	6.3	437	2	Q4ZTV4_PSESY	Q4ztv4	pseudomonas
131	91.5	6.6	732	2	Q9TYJ8_9GENT	Q9tyj8	condaminea	204	88	6.3	500	2	Q9TCC1_NPOLL	Q9tcc1	nephroselm
132	91.5	6.6	1085	2	Q7VQP9_CANBF	Q7vqp9	candidateus	205	88	6.3	524	2	Q4NGA1_9MICC	Q4ngal	arthrobacte
133	91.5	6.6	1221	2	Q4Q6N2_LEIMA	Q4q6n2	leishmania	206	88	6.3	546	2	Q8PXP0_METMA	Q8pxp0	methanosarc
134	91	6.5	257	2	Q6HIW4_BACHK	Q6hiw4	bacillus th	207	88	6.3	622	2	Q7S317_NEUCR	Q7s317	neurospora
135	91	6.5	262	2	Q4NC47_ASPFU	Q4nc47	aspergillus	208	88	6.3	660	2	Q7WMV6_BORBR	Q7wmv6	bordetella
136	91	6.5	340	2	Q5NLU5_ZYMMO	Q5nlus	zymomonas m	209	88	6.3	661	2	Q74F70_GEOSL	Q74f70	geobacter s
137	91	6.5	372	2	Q8NXX5_STAAM	Q8nxes	staphylococ	210	88	6.3	732	2	Q9TJF1_9GENT	Q9tjfl	warzewiczi
138	91	6.5	552	2	Q7WNJ3_BORBR	Q7wnj3	bordetella	211	88	6.3	787	2	Q6SHL0_9BACT	Q6shl0	uncultured
139	90.5	6.5	311	2	Q6CLU8_KLUFLA	Q6clu8	kluveromyc	212	88	6.3	929	2	Q91GCG_ORYSA	Q91gc6	oryza sativ
140	90.5	6.5	337	2	Q4NLG6_9MICC	Q4nlge	arthrobacte	213	88	6.3	1165	1	ADCY6_CANFA	P30804	canis famil
141	90.5	6.5	443	2	Q5JH08_PVRKO	Q5jh08	pyrococcus	214	87.5	6.3	215	2	Q9D2W6_MOUSE	Q9d2w6	mus musculus
142	90.5	6.5	614	2	Q9LNFO_ARATH	Q9lnfo	arabidopsis	215	87.5	6.3	233	1	Y117_BORBU	O51144	borrelia bu
143	90.5	6.5	1505	2	Q73JH5_TREDE	Q73jh5	treponema d	216	87.5	6.3	235	2	Q5NQ68_ZYMMO	Q5nq68	zymomonas m
144	90	6.5	281	2	Q4AJ51_DICDI	Q4aj51	dictyosteli	217	87.5	6.3	300	2	Q5OYH0_ENTHI	Q5oyh0	entamoeba h
145	90	6.5	283	2	Q8NUB1_CORGL	Q8nub1	corynebacte	218	87.5	6.3	361	1	MRAY_LEGPH	Q5zsa2	legionella
146	90	6.5	396	2	Q8FFS3_ECOL6	Q8ffs3	escherichia	219	87.5	6.3	361	1	MRAY_LEGPL	Q5wti4	legionella
147	90	6.5	400	2	Q9KN80_VIBCH	Q9kn80	vibrio chol	220	87.5	6.3	365	2	Q6KH77_MYCMO	Q6khr7	mycoplasma
148	90	6.5	458	2	Q4S023_TETNG	Q4s023	tetraodon n	221	87.5	6.3	427	2	Q4UL81_VICFE	Q4ul81	rickettsia
149	90	6.5	492	1	NUAM_CHOCR	P48915	chondrus cr	222	87.5	6.3	429	2	Q9AKR3_RIBCH	Q9akr3	vibrio chol
150	90	6.5	505	2	Q5AEG5_CANAL	Q5aeg5	candida alb	223	87.5	6.3	432	2	Q68WP9_RICTY	Q68wp9	rickettsia
151	90	6.5	528	1	ATG22_YEAST	P25568	saccharomyc	224	87.5	6.3	453	1	TDE2_MOUSE	Q9qzi8	mus musculus
152	90	6.5	554	2	Q8GJF7_BDEBA	Q8gjf7	bdellovibri	225	87.5	6.3	453	2	Q42W5_9ANNE	Q642w5	clymenella
153	90	6.5	557	2	Q877D2_9CREN	Q877d2	pyrobaculum	226	87.5	6.3	453	2	Q7TNK0_RAT	Q7tnk0	rattus norv
154	90	6.5	669	2	Q5A3N6_CANAL	Q5a3n6	candida alb	227	87.5	6.3	456	2	Q6BQ78_DBBHA	Q6bq78	debaromyce
155	90	6.5	669	2	Q5A3V1_CANAL	Q5a3v1	candida alb	228	87.5	6.3	473	2	Q5PN23_SALPA	Q5pn23	salmonella
156	90	6.5	739	2	Q6MKW0_BDEBA	Q6mkw0	bdellovibri	229	87.5	6.3	482	1	YFIG_BACSU	P54723	bacillus su
157	89.5	6.4	470	2	Q886V4_PSEBSM	Q886v4	pseudomonas	230	87.5	6.3	521	2	Q5X8G4_LEGPA	Q5x8g4	legionella
158	89.5	6.4	437	2	Q9CL14_PASMU	Q9cl14	pasteurella	231	87.5	6.3	530	2	Q8EMR7_OCEIH	Q8emr7	oceanobacil
159	89.5	6.4	440	1	DCUB_HAEIN	P44855	haemophilus	232	87.5	6.3	544	2	O51X57_MAGGR	O51x57	magnaporthe
160	89.5	6.4	440	2	Q6SQD7_MANSM	Q6sqd7	mannheimia	233	87.5	6.3	544	2	O18061_CAEEL	O18061	caenorhabdi
161	89.5	6.4	443	2	Q929T2_LISIN	Q929t2	listeria in	234	87.5	6.3	547	2	Q824X5_CHLCV	Q824x5	chlamydropi
162	89.5	6.4	473	2	Q57LZ5_SALCH	Q57lzs	salmonella	235	87.5	6.3	671	2	Q73WX6_MYCPA	Q73wx6	mycobacteri
163	89.5	6.4	482	2	Q4VIG2_BACCC	Q4vig2	bacillus ce	236	87.5	6.3	732	2	Q9TJQ2_9GENT	Q9tjq2	rustia sple
164	89.5	6.4	485	2	Q88T41_LACPL	Q88t41	lactobacill	237	87.5	6.3	737	2	Q7Q8T7_ANOGA	Q7q8t7	anopheles g
165	89.5	6.4	495	2	O59121_PVBHO	O59121	pyrococcus	238	87.5	6.3	833	2	Q4J5U6_CORJK	Q4j5u6	corynebacte
166	89.5	6.4	521	2	Q5ZYIY_LEGPH	Q5zyi3	legionella	239	87.5	6.3	1687	2	Q6Q117_RAT	Q6q117	rattus norv
167	89.5	6.4	579	2	Q8BDZ0_STRAS	Q8bdzt0	streptococc	240	87	6.2	161	2	Q4S8L4_TETNG	Q4s8l4	tetraodon n
168	89.5	6.4	579	2	Q8E5H7_STRA3	Q8esh7	streptococc	241	87	6.2	257	2	Q4V0X1_BACCC	Q4v0x1	bacillus ce
169	89.5	6.4	599	2	Q22089_CAEEL	Q22089	caenorhabdi	242	87	6.2	261	2	Q7VLV2_HAEDU	Q7vlv2	haemophilus
170	89.5	6.4	963	2	Q7R2T8_GIALA	Q7r2t8	giardia lam	243	87	6.2	269	2	Q41R84_9BURK	Q41r84	burkholderi
171	89	6.4	267	2	Q8BY59_MOUSE	Q8by59	mus musculu	244	87	6.2	271	2	Q6FFL1_ACIAO	Q6ffl1	acinetobact
172	89	6.4	290	2	Q72YR6_BACCI	Q72yr6	bacillus ce	245	87	6.2	396	2	Q8X5A2_ECO57	Q8x5a2	escherichia
173	89	6.4	290	2	Q812M6_BACCR	Q812m6	bacillus ce	246	87	6.2	410	2	Q6ZBS8_BURMA	Q6zbs8	burkholderi
174	89	6.4	428	2	Q8ZJ45_YERPE	Q8zj45	yersinia ps	247	87	6.2	410	2	Q63LLO_BURPS	Q63llo	burkholderi
175	89	6.4	428	2	Q66FK2_YERPS	Q66fk2	yersinia ps	248	87	6.2	412	2	Q4J7I0_SULAC	Q4j7i0	sulfolobus
176	89	6.4	442	2	Q7MP35_VIBVY	Q7mp35	vibrio vuln	249	87	6.2	435	1	EXOO_RHIME	Q03729	rhizobium m
177	89	6.4	637	2	Q9H8H9_HUMAN	Q9h8h9	homo sapien	250	87	6.2	517	2	Q61HG9_CAEBR	Q61hg9	caenorhabdi

251	87	6.2	535	2	Q5WU59_LEGPL	Q5WU59	legionella	324	85.5	6.1	696	2	Q9TIW8_9ASTE	Q9TIW8	phacelia ro
252	87	6.2	535	2	Q5X2E0_LEGPA	Q5X2E0	legionella	325	85.5	6.1	703	2	Q9TLA5_9LAMI	Q9TLA5	jasminum me
253	87	6.2	580	2	Q5AVA3_EMENI	Q5AVA3	aspergillus	326	85.5	6.1	851	2	Q6FU89_CANGA	Q6FU89	candida gla
254	87	6.2	613	2	Q9I4D1_PSEAE	Q9I4D1	pseudomonas	327	85.5	6.1	999	2	Q93JY2_ERWCH	Q93JY2	erwinia chr
255	87	6.2	928	2	Q9LBC9_SOLTU	Q9LBC9	solanum tub	328	85	6.1	304	2	Q96U46_NEUCR	Q96U46	neurospora
256	86.5	6.2	261	2	Q4QK2_HAB18	Q4QK2	haemophilus	329	85	6.1	307	2	Q6P7C6_ACIAD	Q6P7C6	acinetobact
257	86.5	6.2	301	2	Q97OT4_SULTO	Q97OT4	enterococcus	330	85	6.1	333	2	Q6XC99_CYPCA	Q6XC99	corynebacte
258	86.5	6.2	368	2	Q839R1_ENTFA	Q839R1	enterococcus	331	85	6.1	338	1	PSTC1_MYCBO	PSTC1	mycobacteri
259	86.5	6.2	400	1	YCEI_BACSO	Q4WDR2	aspergillus	332	85	6.1	338	1	PSTC1_MYCBO	PSTC1	mycobacteri
260	86.5	6.2	403	2	Q4WDR2_ASFPF	Q4WDR2	aspergillus	333	85	6.1	339	2	Q5L5M5_CHLAB	Q5L5M5	chlamydomphi
261	86.5	6.2	441	2	Q4SY26_TETNG	Q4SY26	tetradon n	334	85	6.1	355	2	Q4L476_STAHL	Q4L476	staphylococ
262	86.5	6.2	544	2	Q4UCA2_THERAN	Q4UCA2	theileria a	335	85	6.1	361	1	MRAY_NITEU	MRAY	nitrosomona
263	86.5	6.2	547	2	Q5L797_CHLAB	Q5L797	chlamydomphi	336	85	6.1	369	2	Q9N2T7_CABEL	Q9N2T7	caenorhabdi
264	86.5	6.2	549	2	Q6N8M3_RHOPA	Q6N8M3	rhodopseudo	337	85	6.1	419	2	Q7PKH1_ANOGA	Q7PKH1	anopheles g
265	86.5	6.2	549	2	Q4KDN8_PSEF5	Q4KDN8	pseudomonas	338	85	6.1	427	2	Q8RKH1_ANOGA	Q8RKH1	anopheles g
266	86.5	6.2	557	2	Q8ZXCL_PYRAE	Q8ZXCL	pyrobaculum	339	85	6.1	443	2	Q9CEP2_LACLA	Q9CEP2	lactococcus
267	86.5	6.2	583	2	Q8Y9B6_LISMO	Q8Y9B6	listeria mo	340	85	6.1	453	1	CAX1B_ORYSA	CAX1B	oryza sativ
268	86.5	6.2	586	2	Q7ZV33_BRARE	Q7ZV33	brachydanio	341	85	6.1	462	2	Q96IE7_SULTO	Q96IE7	sulfolobus
269	86.5	6.2	659	2	Q8MGF7_9DIPS	Q8MGF7	nardostachy	342	85	6.1	497	2	Q6BY36_DEBHA	Q6BY36	debaryomyce
270	86.5	6.2	732	2	Q9TJV8_9GENT	Q9TJV8	chimarthis	343	85	6.1	498	2	Q9QXP0_MOUSE	Q9QXP0	mus musculus
271	86.5	6.2	770	2	Q9YCS4_AERPE	Q9YCS4	aeropyrum p	344	85	6.1	522	2	Q9B8X9_FASHE	Q9B8X9	fasciola he
272	86.5	6.2	1527	2	Q4UD84_THERAN	Q4UD84	theileria a	345	85	6.1	524	2	Q8U4T9_HALVO	Q8U4T9	halobacteri
273	86	6.2	233	2	Q662P5_BORGA	Q662P5	borrelia ga	346	85	6.1	543	2	Q83GL8_TROWT	Q83GL8	tropheryma
274	86	6.2	234	2	Q8R3W1_MOUSE	Q8R3W1	mus musculus	347	85	6.1	543	2	Q83NH2_TROW8	Q83NH2	tropheryma
275	86	6.2	284	2	Q5DBF3_SCHOA	Q5DBF3	schistosoma	348	85	6.1	658	2	Q6XJH9_9ERIC	Q6XJH9	sideroxylon
276	86	6.2	339	2	Q4IEC2_GIBZE	Q4IEC2	gibberella	349	85	6.1	658	2	Q6XJH9_9ERIC	Q6XJH9	sideroxylon
277	86	6.2	372	2	Q6GAU7_STAAS	Q6GAU7	staphylococ	350	85	6.1	845	2	Q8OZ08_MOUSE	Q8OZ08	mus musculus
278	86	6.2	372	2	Q5HHA6_STAAC	Q5HHA6	staphylococ	351	85	6.1	887	2	Q5H6R2_XANOR	Q5H6R2	xanthomonas
279	86	6.2	373	2	Q7A6G2_STAAN	Q7A6G2	staphylococ	352	85	6.1	1166	1	ADCY6_RAT	ADCY6	rattus norv
280	86	6.2	373	2	Q9VBL1_STAAM	Q9VBL1	staphylococ	353	85	6.1	205	2	Q8BL29_MOUSE	Q8BL29	mus musculus
281	86	6.2	389	2	Q9VOC0_PYRAB	Q9VOC0	pyrococcus	354	84.5	6.1	224	2	Q4T540_TETNG	Q4T540	tetradon n
282	86	6.2	396	1	BCR_ECOLI	P28246	escherichia	355	84.5	6.1	269	2	Q837L9_ENTFA	Q837L9	enterococcu
283	86	6.2	444	2	Q7R5W4_9EUCA	Q7R5W4	portunus tr	356	84.5	6.1	283	2	Q6SD18_BACLD	Q6SD18	bacillus li
284	86	6.2	509	2	Q7R5J8_GIUAL	Q7R5J8	giardia lam	357	84.5	6.1	323	2	Q7NXX3_PHOLL	Q7NXX3	photorhabdu
285	86	6.2	667	2	Q8W9Q3_MESVI	Q8W9Q3	mesostigma	358	84.5	6.1	395	2	Q6ND83_RHOPA	Q6ND83	rhodopseudo
286	86	6.2	701	2	Q8HTM4_ACHTR	Q8HTM4	achlys trip	359	84.5	6.1	408	2	Q65FD5_BACLD	Q65FD5	bacillus li
287	86	6.2	703	2	Q9LMM3_ARATH	Q9LMM3	arabidopsis	360	84.5	6.1	405	2	Q7XB13_WHEAT	Q7XB13	tritricum ae
288	86	6.2	725	2	P92949_ARATH	P92949	arabidopsis	361	84.5	6.1	419	2	Q5P123_AOSE	Q5P123	azoarcus sp
289	86	6.2	841	2	Q93QY7_STAXY	Q93QY7	staphylococ	362	84.5	6.1	429	2	Q7Q0F3_ANOGA	Q7Q0F3	anopheles g
290	86	6.2	954	2	Q7VGA9_HELHP	Q7VGA9	helicobacte	363	84.5	6.1	453	1	TDE2_HUMAN	TDE2	homo sapien
291	86	6.2	1308	2	Q8T6H2_DICDI	Q8T6H2	dictyosteli	364	84.5	6.1	453	2	Q9RNX3_RHIEI	Q9RNX3	rhizobium e
292	86	6.2	1328	2	Q5AEK2_DICDI	Q5AEK2	dictyosteli	365	84.5	6.1	461	2	Q5ZME5_CHICK	Q5ZME5	gallus gall
293	86	6.2	1463	2	Q5AVK4_EMENI	Q5AVK4	aspergillus	366	84.5	6.1	463	2	Q66C42_YERPE	Q66C42	versinia ps
294	85.5	6.1	219	2	Q9CY24_MOUSE	Q9CY24	mus musculus	367	84.5	6.1	463	2	Q82FW8_YERPE	Q82FW8	versinia pe
295	85.5	6.1	219	2	Q9D8L7_MOUSE	Q9D8L7	mus musculus	368	84.5	6.1	473	2	Q65N12_BACLD	Q65N12	bacillus li
296	85.5	6.1	250	2	Q6CID8_KIULA	Q6CID8	kluveromyc	369	84.5	6.1	479	2	Q651L0_ORYSA	Q651L0	oryza sativ
297	85.5	6.1	261	2	Q9CP79_PASMO	Q9CP79	pasteurella	370	84.5	6.1	479	2	Q9WZ89_THEMA	Q9WZ89	thermocoga
298	85.5	6.1	295	2	Q5FA38_NEIG1	Q5FA38	neisseria g	371	84.5	6.1	491	2	Q18154_CABEL	Q18154	caenorhabdi
299	85.5	6.1	295	2	Q9K017_NEIMB	Q9K017	neisseria m	372	84.5	6.1	515	2	Q9LN48_ARATH	Q9LN48	arabidopsis
300	85.5	6.1	296	2	Q669X3_YERPE	Q669X3	versinia ps	373	84.5	6.1	562	2	Q9FLI8_ARATH	Q9FLI8	arabidopsis
301	85.5	6.1	296	2	Q82F11_YERPE	Q82F11	versinia pe	374	84.5	6.1	589	2	Q95ZY6_CABEL	Q95ZY6	caenorhabdi
302	85.5	6.1	311	1	PAQR3_HUMAN	Q6TCH7	homo sapien	375	84.5	6.1	638	2	Q33749_ARBLI	Q33749	arabacia lix
303	85.5	6.1	311	2	Q88TD9_LACPL	Q88TD9	lactobacill	376	84.5	6.1	671	2	Q55T80_CRYNE	Q55T80	cryptococcu
304	85.5	6.1	329	2	Q96K55_HUMAN	Q96K55	homo sapien	377	84.5	6.1	674	2	Q5KJ61_CRYNE	Q5KJ61	cryptococcu
305	85.5	6.1	355	2	Q8TNPX8_METAC	Q8TNPX8	methanosarc	378	84.5	6.1	702	2	Q9TLF1_9LAMI	Q9TLF1	lindenbergi
306	85.5	6.1	399	2	Q75PY5_CAVPO	Q75PY5	cavia porce	379	84.5	6.1	913	2	Q7UJ14_RHOBA	Q7UJ14	rhodopirell
307	85.5	6.1	401	2	Q89KV1_BRAJA	Q89KV1	bradyrhizob	380	84.5	6.1	1982	2	Q4Q897_LEIMA	Q4Q897	leishmania
308	85.5	6.1	453	2	Q5R419_PONPY	Q5R419	pongo pygma	381	84	6.0	172	2	Q9TA01_LAMFL	Q9TA01	lametra fl
309	85.5	6.1	453	2	Q5R4G3_PONPY	Q5R4G3	pongo pygma	382	84	6.0	234	2	Q99N04_MOUSE	Q99N04	mus musculus
310	85.5	6.1	470	2	Q4T836_TETNG	Q4T836	tetradon n	383	84	6.0	295	2	Q7YFS4_9HYME	Q7YFS4	neivamyrmex
311	85.5	6.1	482	2	Q4S426_TETNG	Q4S426	tetradon n	384	84	6.0	318	2	Q97NY1_STRPN	Q97NY1	streptococc
312	85.5	6.1	496	2	Q5ZMS7_CHICK	Q5ZMS7	gallus gall	385	84	6.0	329	2	Q8U0A2_PYRFU	Q8U0A2	pyrococcus
313	85.5	6.1	498	2	Q21287_RECAM	Q21287	reclinomona	386	84	6.0	403	2	Q7MUU1_PORGI	Q7MUU1	porphyromon
314	85.5	6.1	521	2	Q8WUB5_HUMAN	Q8WUB5	homo sapien	387	84	6.0	408	2	Q8JMR3_TROWT	Q8JMR3	tropheryma
315	85.5	6.1	526	2	Q9OX46_BRARE	Q9OX46	brachydanio	388	84	6.0	408	2	Q8JN96_TROW8	Q8JN96	tropheryma
316	85.5	6.1	528	2	Q6A2J4_9LAMI	Q6A2J4	brandisia h	389	84	6.0	448	2	Q5YTA9_NOCFA	Q5YTA9	nocardia fa
317	85.5	6.1	545	2	Q96JZ5_HUMAN	Q96JZ5	homo sapien	390	84	6.0	459	2	Q529R6_ORYSA	Q529R6	oryza sativ
318	85.5	6.1	572	2	Q4XZG8_PLACH	Q4XZG8	plasmodium	391	84	6.0	460	2	O59186_PYRHO	O59186	pyrococcus
319	85.5	6.1	587	1	TM9S3_MOUSE	Q9ETJ0	mus musculus	392	84	6.0	464	2	Q518J3_ENTHI	Q518J3	entamoeba h
320	85.5	6.1	589	1	TM9S3_HUMAN	Q9H457	homo sapien	393	84	6.0	465	2	Q4ZFM6_PSESY	Q4ZFM6	pseudomonas
321	85.5	6.1	589	2	Q5TB57_HUMAN	Q5TB57	homo sapien	394	84	6.0	478	2	Q74FM6_PSESY	Q74FM6	pseudomonas
322	85.5	6.1	629	2	Q571B0_MOUSE	Q571B0	mus musculus	395	84	6.0	575	2	Q91642_PSEAE	Q91642	pseudomonas
323	85.5	6.1	682	2	Q83C62_COXBU	Q83C62	coxiella bu	396	84	6.0	597	2	Q9KUW6_VIBCH	Q9KUW6	vibrio chol

397	84	6.0	599	2	Q61Z28 CABER	Q61Z28 caenorhabdi	470	82.5	5.9	486	2	Q82YJ7 ENTFA	Q82YJ7 enterococc
398	84	6.0	602	2	Q50S30 MACLA	Q5G830 macroctis la	471	82.5	5.9	494	1	NU4M TRIRU	Q36834 trichophyto
399	84	6.0	679	2	Q511J8 ENTHI	Q511J8 entamoeba h	472	82.5	5.9	508	2	Q950R5 SIPFN	Q350R5 spizellomyc
400	84	6.0	679	2	Q518I7 ENTHI	Q518I7 entamoeba h	473	82.5	5.9	543	2	Q7Z5I7 HUMAN	Q7Z5I7 homo sapien
401	84	6.0	736	2	Q9TJ51_9GENT	Q9TJ51 paucidianth	474	82.5	5.9	548	1	Q6AAJ7 PROAC	P380J7 propionibac
402	84	6.0	830	2	Q6C772 YARLI	Q6C772 yarrowia li	475	82.5	5.9	596	1	AGP2 YEAST	P38090 saccharomyc
403	84	6.0	935	2	Q9ZP04_TROMA	Q9ZP04 tropaeolum	476	82.5	5.9	620	2	Q7S5R8 NEUCR	Q7S5R8 neurospora
404	84	6.0	4083	1	DYHC ASHGO	D9C1M7 ashbya goss	477	82.5	5.9	623	2	Q98P35_RHILO	Q98P35 rhizobium 1
405	83.5	6.0	261	1	Y1086_HAEIN	P45030 haemophilus	478	82.5	5.9	636	2	Q5KS83_9SCHI	Q5KS83 luidia quin
406	83.5	6.0	295	2	Q9JUV1_NEIMA	Q9JUV1 neisseria m	479	82.5	5.9	640	2	Q6MB47_PASHUW	Q6MB47 parachlamyd
407	83.5	6.0	311	2	Q4R6X2_MACFA	Q4R6X2 macaca fasc	480	82.5	5.9	671	2	Q751I3 ASHGO	Q751I3 ashbya goss
408	83.5	6.0	324	2	Q8XX91_RALSO	Q8XX91 ralstonia s	481	82.5	5.9	680	2	Q70SP4_9IAMI	Q70SP4 limosella m
409	83.5	6.0	330	2	Q8AA46_BACTN	Q8AA46 bacteroides	482	82.5	5.9	680	2	Q8SL84_9DIPS	Q8SL84 nardostachy
410	83.5	6.0	333	2	Q8BA46_STR43	Q8BA46 streptococc	483	82.5	5.9	704	2	Q9SCD0_9ERIC	Q9SCD0 gustavia su
411	83.5	6.0	468	2	Q8XYK8_CLOPE	Q8XYK8 clostridium	484	82.5	5.9	733	2	Q9VXB8_ORYGA	Q9VXB8 cryza sativ
412	83.5	6.0	480	2	Q5DYP6_VIBF1	Q5DYP6 vibrio fisc	485	82.5	5.9	1121	2	Q4T7Y0_TETNG	Q4T7Y0 tetraodon n
413	83.5	6.0	481	2	Q4RQ81_TETNG	Q4RQ81 tetraodon n	486	82.5	5.9	1363	2	Q7PPE3_ANOGA	Q7PPE3 anopheles g
414	83.5	6.0	509	2	Q8IA95_CABEL	Q8IA95 caenorhabdi	487	82.5	5.9	1457	2	Q9HCE0_HUMAN	Q9HCE0 homo sapien
415	83.5	6.0	521	1	YJBC SCHPO	Q74949 schizosacch	488	82	5.9	219	2	Q752S0_HUMAN	Q752S0 homo sapien
416	83.5	6.0	521	2	Q87557_SACKL	Q87557 saccharomyc	489	82	5.9	267	2	Q88HZ2_PSEPK	Q88HZ2 pseudomonas
417	83.5	6.0	531	2	Q83EAO_COXBU	Q83EAO coxiella bu	490	82	5.9	299	1	T2R18_FAT	Q9JKU0 rattus norv
418	83.5	6.0	605	2	Q9L1F6_STRCO	Q9L1F6 streptomyc	491	82	5.9	313	2	Q87GV0_VIBPA	Q87GV0 vibrio para
419	83.5	6.0	638	1	NUSM_PARLI	P12176 paracentrot	492	82	5.9	317	2	Q9K6Y6_BACHPD	Q9K6Y6 bacillus ha
420	83.5	6.0	693	2	Q4WCR6_9DIPS	Q4WCR6 nardostachy	493	82	5.9	327	2	Q9KT03_VIBCH	Q9KT03 vibrio chol
421	83.5	6.0	735	2	Q4WCR6_ASFPU	Q4WCR6 aspergillus	494	82	5.9	339	2	Q84ET2_9PROC	Q84ET2 uncultured
422	83.5	6.0	736	2	Q9TJZ7_9ASTE	Q9TJZ7 anthospermu	495	82	5.9	347	2	Q4IU66_AZOV1	Q4IU66 azotobacter
423	83.5	6.0	743	2	Q8WH76_9ASTE	Q8WH76 forgesia ra	496	82	5.9	356	2	Q9FZ96_ARATH	Q9FZ96 arabidopsis
424	83.5	6.0	976	2	Q6FXK3_CANGA	Q6FXK3 candida gla	497	82	5.9	356	2	Q9M7R1_ARATH	Q9M7R1 arabidopsis
425	83.5	6.0	1829	2	Q86HD9_DICDI	Q86HD9 dictyosteli	498	82	5.9	359	2	Q97C50_THEVO	Q97C50 thermoplasma
426	83.5	6.0	1867	2	Q551P7_DICDI	Q551P7 dictyosteli	499	82	5.9	365	2	Q5M7L7_XENTR	Q5M7L7 xenopus tro
427	83	6.0	241	2	Q5UPE7_MIMIV	Q5UPE7 mimivirus.	500	82	5.9	389	2	Q25590_HELPU	Q25590 helicobacte
428	83	6.0	297	2	Q4KA95_PSEF5	Q4KA95 pseudomonas	501	82	5.9	405	2	Q983X3_RHILO	Q983X3 rhizobium 1
429	83	6.0	305	2	Q8YWR6_ANASP	Q8YWR6 anabaena sp	502	82	5.9	412	2	Q5IA38_AMBTC	Q5IA38 amborella t
430	83	6.0	318	2	Q8DNJ4_STRR6	Q8DNJ4 streptococc	503	82	5.9	446	1	CITN_KLEPN	P31602 klebsiella
431	83	6.0	321	1	ORSV1_HUMAN	Q9UGF6 homo sapien	504	82	5.9	459	2	Q70XF0_DROAU	Q70XF0 dromiciops
432	83	6.0	321	2	Q5SQ19_HUMAN	Q5SQ19 homo sapien	505	82	5.9	465	2	Q74M77_NANEQ	Q74M77 nanoarchaeu
433	83	6.0	321	2	Q6NTB5_HUMAN	Q6NTB5 homo sapien	506	82	5.9	488	2	Q93YP9_ARATH	Q93YP9 arabidopsis
434	83	6.0	324	2	Q4X186_ASFPU	Q4X186 aspergillus	507	82	5.9	494	2	Q6F0R2_MESFL	Q6F0R2 mesoplasma
435	83	6.0	427	2	Q7F8Q1_RICSI	Q7F8Q1 rickettsia	508	82	5.9	497	2	Q97A43_THEVO	Q97A43 thermoplasma
436	83	6.0	427	2	Q92HP5_RICCN	Q92HP5 rickettsia	509	82	5.9	498	2	Q73GW3_WOLPM	Q73GW3 wolbachia p
437	83	6.0	457	2	Q8UIE5_PYRFU	Q8UIE5 pyrococcus	510	82	5.9	514	2	Q4LNM2_9BURK	Q4LNM2 burkholderi
438	83	6.0	460	2	Q9VOY7_PYRAB	Q9VOY7 pyrococcus	511	82	5.9	545	2	Q8FNV5_COREF	Q8FNV5 corynebacte
439	83	6.0	466	2	Q7VNG8_HAEMPH	Q7VNG8 haemophilus	512	82	5.9	548	2	Q9A8F3_CAUCR	Q9A8F3 caulobacter
440	83	6.0	467	2	Q6F9F8_ACIAD	Q6F9F8 acinetobact	513	82	5.9	557	1	YQ04_SCHPO	Q74537 schizosacch
441	83	6.0	496	2	Q914I8_PSEAE	Q914I8 pseudomonas	514	82	5.9	557	2	Q8G3S6_BIFLO	Q8G3S6 bifidobacte
442	83	6.0	587	2	Q87T28_PSESM	Q87T28 pseudomonas	515	82	5.9	573	2	Q99932_CABEL	Q99932 caenorhabdi
443	83	6.0	637	1	NUSM_STRPU	P15552 strongyloce	516	82	5.9	594	2	Q7T709_9CLOS	Q7T709 citrus tris
444	83	6.0	802	2	Q8SZ78_DROME	Q8SZ78 drosophila	518	82	5.9	706	2	Q45283_CABEL	Q45283 caenorhabdi
445	83	6.0	1139	2	Q6SD06_YERPS	Q6SD06 yersinia ps	519	82	5.9	727	2	Q5A438_CANAL	Q5A438 candida alb
446	83	6.0	1835	2	Q9C1I7_MYCGR	Q9C1I7 mycosphaere	520	82	5.9	748	2	Q6N6C2_PROAC	Q6N6C2 propionibac
447	83	6.0	2159	2	Q8RUQ1_MAIZE	Q8RUQ1 zea mays (m	521	82	5.9	881	2	Q6F8D1_ACIAD	Q6F8D1 acinetobact
448	83	6.0	2159	2	Q8RVL1_MAIZE	Q8RVL1 zea mays (m	522	82	5.9	884	2	Q8ER30_OCEIH	Q8ER30 oceanobacil
449	83	6.0	2220	2	Q52FU9_MAGGR	Q52FU9 magnaporthe	523	82	5.9	893	2	Q511Z0_ENTHI	Q511Z0 entamoeba h
450	83	6.0	2220	2	Q52FU9_MAGGR	Q52FU9 magnaporthe	523	82	5.9	1029	2	Q6KAN9_MOUSE	Q6KAN9 mus musculu
451	82.5	5.9	281	2	Q83BV7_COXBU	Q83BV7 coxiella bu	524	82	5.9	1139	2	Q8ZC91_YBRPE	Q8ZC91 yersinia pe
452	82.5	5.9	337	2	Q59QT6_CANAL	Q59QT6 candida alb	525	82	5.9	1156	2	Q74WP6_YERPE	Q74WP6 yersinia pe
453	82.5	5.9	346	2	Q8TQ84_METAC	Q8TQ84 mechanosarc	526	82	5.9	1168	1	ADCY6_HUMAN	Q43306 homo sapien
454	82.5	5.9	368	2	Q72KY8_THET2	Q72KY8 thermus the	527	81.5	5.9	205	2	Q8CYE9_STRR6	Q8CYE9 streptococc
455	82.5	5.9	391	1	EPT1_YEAST	P221Y8 saccharomyc	528	81.5	5.9	205	2	Q97PC0_STRPN	Q97PC0 streptococc
456	82.5	5.9	400	2	Q7M916_WOLSU	Q7M916 wolinnella s	529	81.5	5.9	268	2	Q8D9M9_VIBVU	Q8D9M9 vibrio vuln
457	82.5	5.9	402	2	Q4HYV9_GIBZE	Q4HYV9 gibberella	530	81.5	5.9	268	2	Q7MKQ7_VIBVU	Q7MKQ7 vibrio vuln
458	82.5	5.9	418	2	Q9HXM9_PSEAE	Q9HXM9 pseudomonas	531	81.5	5.9	292	2	Q4JT26_CORJK	Q4JT26 corynebacte
459	82.5	5.9	432	2	Q5PE07_SALPA	Q5PE07 salmonella	532	81.5	5.9	292	2	Q92DGO_LISIN	Q92DGO listeria in
460	82.5	5.9	437	2	Q81KE3_PLAF7	Q81KE3 plasmodium	533	81.5	5.9	307	1	UPPP2_CLOAB	Q97Kf6 clostridium
461	82.5	5.9	439	2	Q4UYJ1_XANCP	Q4UYJ1 xanthomonas	534	81.5	5.9	325	2	Q94VH0_VARGO	Q94VH0 varanus gou
462	82.5	5.9	439	2	Q8P5I4_XANCP	Q8P5I4 xanthomonas	535	81.5	5.9	325	2	Q973Q6_SULTO	Q973Q6 sulfolobus
463	82.5	5.9	448	2	Q6DVM4_9CRUS	Q6DVM4 triops long	536	81.5	5.9	351	2	Q9FZ95_ARATH	Q9FZ95 arabidopsis
464	82.5	5.9	451	2	Q82CI8_STRAM	Q82CI8 streptomyc	537	81.5	5.9	390	2	Q5BDJ8_EWENI	Q5BDJ8 aspergillus
465	82.5	5.9	452	2	Q9ZKR4_HELPJ	Q9ZKR4 helicobacte	538	81.5	5.9	399	2	Q8NCC4_HUMAN	Q8NCC4 homo sapien
466	82.5	5.9	453	2	Q5RCN8_PONPY	Q5RCN8 pongo pygma	539	81.5	5.9	410	2	Q5NGS9_FRATT	Q5NGS9 francisella
467	82.5	5.9	462	2	Q6F0L1_MESFL	Q6F0L1 mesoplasma	540	81.5	5.9	425	2	Q88CV8_PSEPK	Q88CV8 pseudomonas
468	82.5	5.9	471	2	Q88SS9_LACPL	Q88SS9 lactobacill	541	81.5	5.9	435	2	Q4YAK0_PLABE	Q4YAK0 plasmodium
469	82.5	5.9	478	2	Q8EEL5_SHEON	Q8EEL5 shewanella	542	81.5	5.9	436	2	Q7YZ03_CRYPV	Q7YZ03 cryptospori

543	81.5	5.9	438	2	Q9HVD9_PSEAB	Q9hud9 pseudomonas	616	80.5	5.8	261	2	Q6LTB2_PHOPR	Q6ltb2 photobacter
544	81.5	5.9	446	2	Q6OWD5_CAEBR	Q6owd5 caenorhabdi	617	80.5	5.8	288	2	Q85JA0_CLOSI	Q85ja0 clostrichis
545	81.5	5.9	454	2	Q4ZVE0_PSESY	Q4zve0 pseudomonas	618	80.5	5.8	291	2	Q746X4_GEOSL	Q746x4 geobacter s
546	81.5	5.9	454	2	Q88AR2_PSESM	Q88ar2 pseudomonas	619	80.5	5.8	316	2	Q647F8_VIRUR	Q647f8 thermoprote
547	81.5	5.9	454	2	Q89WU1_BRAJA	Q89wu1 bradyrhizob	620	80.5	5.8	321	2	Q94VDA_9SAUR	Q94vda varanus pan
548	81.5	5.9	463	2	Q5DBJ2_SCHJA	Q5dbj2 schistosoma	621	80.5	5.8	324	2	Q83ZG6_9GAWM	Q83z26 lamprocysti
549	81.5	5.9	467	2	Q9W1Z2_DROME	Q9w1z2 drosophila	622	80.5	5.8	333	2	Q81HX6_PLAF7	Q81hx6 plasmodium
550	81.5	5.9	485	2	Q8SYB7_DROME	Q8syb7 drosophila	623	80.5	5.8	334	2	Q8AWL9_DROME	Q8awl9 drosophila
551	81.5	5.9	485	2	Q9W1Z3_DROME	Q9w1z3 drosophila	624	80.5	5.8	334	2	Q8IQJ7_DROME	Q8iqj7 drosophila
552	81.5	5.9	485	2	Q18063_CAEBL	Q18063 caenorhabdi	625	80.5	5.8	359	2	Q6G6F7_STAAS	Q6g6f7 staphylococ
553	81.5	5.9	487	2	Q4TN74_9SPHN	Q4tn74 erythroba	626	80.5	5.8	359	2	Q5HD36_STAAC	Q5hd36 staphylococ
554	81.5	5.9	510	2	Q34523_FASHE	Q34523 fasciola he	627	80.5	5.8	359	2	Q79ZZ9_STAAN	Q79zz9 staphylococ
555	81.5	5.9	517	2	Q4HUN6_GIBZE	Q4hun6 gibberella	628	80.5	5.8	359	2	Q7A314_STAAN	Q7a314 staphylococ
556	81.5	5.9	524	2	Q4SNU4_TETNG	Q4snu4 tetraodon n	629	80.5	5.8	359	2	Q99RB8_STAAN	Q99rb8 staphylococ
557	81.5	5.9	535	2	Q53111_RHOSH	Q53111 rhodobacter	630	80.5	5.8	360	2	Q7Q2N8_ANOGA	Q7q2n8 anopheles g
558	81.5	5.9	618	2	Q5AY73_EMENI	Q5ay73 aspergillus	631	80.5	5.8	366	2	Q8CWZ5_STRMU	Q8cwz5 streptococ
559	81.5	5.9	623	2	Q519X5_ENTHI	Q519x5 entamoeba h	632	80.5	5.8	368	2	Q610H8_CAEBR	Q610h8 caenorhabdi
560	81.5	5.9	626	2	Q8XUM7_RALSO	Q8xum7 ralstonia s	633	80.5	5.8	373	2	Q5YN20_NOCFA	Q5yn20 nocardia fa
561	81.5	5.9	711	2	Q6LH73_PHOPR	Q6lh73 photobacter	634	80.5	5.8	393	2	Q5HM49_STAEP	Q5hm49 staphylococ
562	81.5	5.9	713	2	Q9VWG4_DROME	Q9vwg4 drosophila	635	80.5	5.8	393	2	Q8CNG2_STAEP	Q8cng2 staphylococ
563	81.5	5.9	724	2	Q8MRA8_DROME	Q8mra8 drosophila	636	80.5	5.8	419	2	Q81NE5_BACAN	Q81ne5 bacillus an
564	81.5	5.9	724	2	Q9TJZ6_9GENT	Q9tjz6 alsais lugo	637	80.5	5.8	433	2	Q74XD2_YERPE	Q74xd2 yersinia pe
565	81.5	5.9	731	2	Q9TJZ7_9GENT	Q9tjz7 hillia trif	638	80.5	5.8	433	2	Q821Y7_YERPE	Q821y7 yersinia pe
566	81.5	5.9	732	2	Q9TJZ8_9GENT	Q9tjz8 pogonopus s	639	80.5	5.8	433	2	Q66FD9_YERPS	Q66fd9 yersinia ps
567	81.5	5.9	734	2	Q98706_9GENT	Q98706 chlocoeca r	640	80.5	5.8	438	2	Q87VV4_PSESM	Q87vv4 pseudomonas
568	81.5	5.9	741	2	Q71QV9_9ASTR	Q71qv9 siegesbecki	641	80.5	5.8	446	2	Q951C1_TETTH	Q951c1 tetrahymena
569	81.5	5.9	745	2	Q5UYV6_HALMA	Q5uyv6 haloarcula	642	80.5	5.8	453	2	Q618Q8_CAEBR	Q618q8 caenorhabdi
570	81.5	5.9	855	2	Q6BGA9_PARTE	Q6bga9 paramecium	643	80.5	5.8	454	2	Q4K8P3_PSEF5	Q4k8p3 pseudomonas
571	81.5	5.9	893	2	Q548C6_DICDI	Q548c6 dictyosteli	644	80.5	5.8	469	2	Q93561_SOLTU	Q93561 solanum tub
572	81.5	5.9	1402	2	Q610A1_CAEBR	Q610a1 caenorhabdi	645	80.5	5.8	470	2	Q9CP91_PASMU	Q9cp91 pasteurella
573	81	5.8	226	2	Q4MWG5_BACCE	Q4mwg5 bacillus ce	646	80.5	5.8	472	2	Q4LSU9_9BURK	Q4lsu9 burkholderi
574	81	5.8	226	2	Q816R9_BACCR	Q816r9 bacillus ce	647	80.5	5.8	473	1	IOLT_BACSU	Iolt718 bacillus su
575	81	5.8	228	2	Q4L948_STAHT	Q4l948 staphylococ	648	80.5	5.8	475	2	Q6LR41_PHOPR	Q6lr41 photobacter
576	81	5.8	287	2	Q5V2C4_HALMA	Q5v2c4 haloarcula	649	80.5	5.8	523	2	Q8AA31_BACTN	Q8aa31 bacteroides
577	81	5.8	293	1	Y417_CHLTR	Q84422 chlamydia t	650	80.5	5.8	528	2	Q5F6U6_NEIG1	Q5f6u6 neisseria g
578	81	5.8	293	2	Q92WD8_RHIME	Q92wd8 rhizobium m	651	80.5	5.8	528	2	Q9JRD7_NEIMA	Q9jrd7 neisseria m
579	81	5.8	297	2	Q5NMK8_ZYMON	Q5nmk8 zymomonas m	652	80.5	5.8	528	2	Q7DDN3_NEIMB	Q7ddn3 neisseria m
580	81	5.8	305	2	Q5J3L3_RAT	Q5j3l3 rattus norv	653	80.5	5.8	531	2	Q6KI84_MYCMO	Q6ki84 mycoplasma
581	81	5.8	313	1	RBN_VIBVU	Q8dd62 vibrio vuln	654	80.5	5.8	536	2	Q6MEN5_PARUM	Q6men5 paracitlamyd
582	81	5.8	313	1	RBN_VIBVY	Q7mg07 vibrio vuln	655	80.5	5.8	590	1	CAN1_YEAST	P04817 saccharomyc
583	81	5.8	375	2	P95505_PROHO	P95505 prochloroth	656	80.5	5.8	637	2	O21277_RECAM	O21277 reclinomona
584	81	5.8	375	2	Q95PD7_ZYMON	Q95pd7 zymomonas m	657	80.5	5.8	660	2	Q891N8_CLOTE	Q891n8 clostridium
585	81	5.8	382	2	Q918P4_CYPCL	Q918p4 cyprinus ca	658	80.5	5.8	690	2	Q4NU84_9BELT	Q4nu84 anaeromyxob
586	81	5.8	396	2	Q83KE0_SHIFL	Q83ke0 shigella fl	659	80.5	5.8	728	2	Q98702_9GENT	Q98702 luculia gra
587	81	5.8	422	2	Q6ESP5_ORYSA	Q6esp5 oryza sativ	660	80.5	5.8	732	2	Q9TJY9_CALCA	Q9tjy9 calycophyll
588	81	5.8	422	2	Q8Y1K4_RALSO	Q8y1k4 ralstonia s	661	80.5	5.8	812	2	Q55KN8_CRYNE	Q55kn8 cryptococcu
589	81	5.8	438	2	Q8X4U5_ECO57	Q8x4u5 escherichia	662	80.5	5.8	812	2	Q5KAT6_CRYNE	Q5kat6 cryptococcu
590	81	5.8	461	1	YCUJ_ECOLI	P76037 escherichia	663	80.5	5.8	834	1	SL9A3_HUMAN	P48764 homo sapien
591	81	5.8	471	2	Q483Y1_TETNG	Q483y1 tetraodon n	664	80	5.7	210	2	Q5VWV7_HUMAN	Q5vww7 homo sapien
592	81	5.8	479	2	Q87155_VIBCH	Q87155 vibrio chol	665	80	5.7	226	2	Q81KJ3_BACAN	Q81kj3 bacillus an
593	81	5.8	479	2	Q5H778_ECOLI	Q5h778 escherichia	666	80	5.7	266	2	Q9HXP7_PGEAE	Q9hxp7 pseudomonas
594	81	5.8	483	2	Q62AN5_CAEBR	Q62an5 caenorhabdi	667	80	5.7	268	2	Q76FP9_STYPL	Q76fp9 stytela plic
595	81	5.8	485	2	Q7POT4_ANOGA	Q7pot4 anopheles g	668	80	5.7	270	2	Q5JB18_PPRKO	Q5jb18 pyrococcus
596	81	5.8	487	2	Q9FRL3_ARATH	Q9frl3 arabidopsis	669	80	5.7	277	2	Q818H6_BACCR	Q818h6 bacillus ce
597	81	5.8	515	2	Q8TF71_HUMAN	Q8tf71 homo sapien	670	80	5.7	285	2	Q6YQJ4_ONYPE	Q6yqj4 onion yello
598	81	5.8	544	1	YRT3_CAEBL	Q10046 caenorhabdi	671	80	5.7	286	2	Q4MMH9_BACCE	Q4mmh9 bacillus ce
599	81	5.8	548	2	Q8AAZ9_BACTN	Q8aaz9 bacteroides	672	80	5.7	286	2	Q81RV2_BACAN	Q81rv2 bacillus an
600	81	5.8	550	2	Q7NZQ0_CHRVO	Q7nq0 chromobacte	673	80	5.7	286	2	Q6HK25_BACHK	Q6hk25 bacillus th
601	81	5.8	595	2	Q91MJ8_9PARA	Q91mj8 menangia vi	674	80	5.7	286	2	Q63CM0_BACCZ	Q63cm0 bacillus ce
602	81	5.8	608	2	Q7QP79_GIALA	Q7qp79 giardia lam	675	80	5.7	289	2	Q8UVU0_MIMPU	Q8dvv0 mimosa pudl
603	81	5.8	647	2	Q9GEU0_SAMVA	Q9geu0 samolus val	676	80	5.7	291	2	Q8UIQ9_AGRT5	Q8uiq9 agrobacteri
604	81	5.8	657	2	Q6XJ11_9ERIC	Q6xj11 sideroxylon	677	80	5.7	296	2	Q4MPJ0_BACCE	Q4mpj0 bacillus ce
605	81	5.8	710	2	O19824_9LAMI	O19824 cobanathus	678	80	5.7	299	2	Q6AL50_DSPPS	Q6al50 deulfofale
606	81	5.8	724	2	Q9GF06_9ERIC	Q9gf06 bonellia um	679	80	5.7	322	2	Q9GEH0_9MYRT	Q9geh0 menecylon b
607	81	5.8	734	2	Q9THV8_9GENT	Q9thv8 rondeletia	680	80	5.7	339	2	Q84ETI_9PROC	Q84eti prochloroth
608	81	5.8	743	2	Q61LV8_CAEBR	Q61lv8 caenorhabdi	681	80	5.7	363	2	Q8KR39_CLOSJ	Q8kr39 clostridium
609	81	5.8	875	2	Q9V8U1_DROME	Q9v8u1 drosophila	682	80	5.7	364	2	Q5I723_BACNO	Q5i723 bacteroides
610	81	5.8	889	2	Q4V5E4_DROME	Q4v5e4 drosophila	683	80	5.7	380	2	Q4RMW9_TETNG	Q4rmw9 tetraodon n
611	81	5.8	971	2	Q68XX4_RICTY	Q68xx4 rickettsia	684	80	5.7	386	2	Q4NM07_BACCE	Q4nm07 bacillus ce
612	81	5.8	1102	2	Q88CW3_PSEPK	Q88cw3 pseudomonas	685	80	5.7	387	2	Q55IJ1_CRYNE	Q55ij1 cryptococcu
613	81	5.8	1207	2	Q4P6A9_USTWA	Q4p6a9 ustilago ma	686	80	5.7	391	2	Q6LY81_CRYNE	Q6ly81 methanococ
614	81	5.8	2186	1	POLG_CXB20	Q9y1g5 c genome po	687	80	5.7	409	2	Q4KK15_PSEF5	Q4kk15 pseudomonas
615	80.5	5.8	162	2	Q7NN16_GLOVI	Q7nn16 gloebacter	688	80	5.7	429	1	ARSB_STAAU	P30329 staphylococ

689	80	5.7	429	2	Q9AC73_STAAN	Q9ac73	staphylococ	762	79.5	5.7	593	2	Q5BM61_DBBHA	Q6bm61	debaryomyce
690	80	5.7	439	2	Q8PGX4_XANAC	Q8pgx4	xanthomonas	763	79.5	5.7	596	2	Q5Z6S8_ORYSA	Q5z6s8	oryza sativ
691	80	5.7	445	2	Q6NF01_CORDI	Q6nf01	corynebacte	764	79.5	5.7	598	2	Q7CZ11_AGRIT5	Q7cz11	agrobacter1
692	80	5.7	450	2	Q4WZY0_THEPA	Q4mzy0	theileria p	765	79.5	5.7	600	2	Q6LKCO_PROPR	Q6lkco	photobacter
693	80	5.7	451	2	Q617X8_LEPDU	Q617x8	leptotophilo	766	79.5	5.7	613	2	Q8CBQ1_MWYTH	Q8cbq1	mus musculu
694	80	5.7	472	2	Q9N5Q8_CABEL	Q9n5q8	caenorhabdi	767	79.5	5.7	628	2	Q67ML1_SYMTH	Q67ml1	symbiobacte
695	80	5.7	488	2	Q55GU7_DICDI	Q55gu7	dictyosteli	768	79.5	5.7	632	2	Q9AZ47_BSP6	Q9az47	enterobacte
696	80	5.7	488	2	Q966D7_CABEL	Q966d7	caenorhabdi	769	79.5	5.7	639	2	Q5WC83_BACSK	Q5wc83	bacillus cl
697	80	5.7	512	2	Q4WFT2_ASPFU	Q4wft2	aspergillus	770	79.5	5.7	669	2	Q6USQ3_9DIPS	Q6usq3	valeriana e
698	80	5.7	516	2	Q4OJG1_ORYSA	Q4ojg1	oryza sativ	771	79.5	5.7	677	2	Q6CY48_KULU	Q6cy48	kluyveromyc
699	80	5.7	528	2	Q5OZV7_ENTHI	Q5ozv7	entamoeba h	772	79.5	5.7	695	2	Q9TJS9_9GENT	Q9tjs9	mussaenda a
700	80	5.7	558	2	Q6XRA4_9BACT	Q6xra4	uncultured	773	79.5	5.7	697	2	Q6YSA9_ORYSA	Q6ysa9	oryza sativ
701	80	5.7	657	2	Q6XJM6_9ERIC	Q6xjm6	inhamaneill	774	79.5	5.7	699	2	Q91YL7_MOUSE	Q91yl7	mus musculu
702	80	5.7	671	2	Q7WXB7_ALCEU	Q7wbx7	alcaligenes	775	79.5	5.7	734	2	Q4RWS7_TETNG	Q4rws7	tetradodon n
703	80	5.7	699	2	Q9TIF3_9LAMI	Q9tif3	hemiphragma	776	79.5	5.7	741	2	Q32132_9ASTR	Q32132	chrysanthem
704	80	5.7	702	2	Q19823_9ALOB	Q19823	alobesia sp.	777	79.5	5.7	831	1	SL9A3_RAT	P26433	rattus norv
705	80	5.7	714	2	Q73Y59_MYCPA	Q73y59	mycobacteri	778	79.5	5.7	876	2	Q8MKL0_DROME	Q8mklo	drosophila
706	80	5.7	740	2	Q9TJU4_CEOPO	Q9tju4	cephalanthu	779	79.5	5.7	976	2	Q96VU4_BURPS	Q96vu4	blumeria gr
707	80	5.7	740	2	Q5PG25_SALPA	Q5pg25	salmonella	780	79.5	5.7	1078	2	Q5SF45_DICDI	Q5sf45	dictyosteli
708	80	5.7	740	2	Q8ZQN3_SALTY	Q8zqn3	salmonella	781	79.5	5.7	1321	2	Q4RSL1_TETNG	Q4rsl1	tetradodon n
709	80	5.7	902	2	Q9K9X9_BACHD	Q9k9x9	bacillus ha	782	79.5	5.7	1529	2	Q5HB09_EHRRW	Q5hb09	ehrllichia r
710	80	5.7	1067	2	Q8EJ80_SHEON	Q8ej80	shewanella	783	79.5	5.7	1539	2	Q4UE92_THEAN	Q4ue92	theileria a
711	80	5.7	1123	2	Q91YR7_ARATH	Q91yr7	arabidopsis	784	79.5	5.7	1569	2	Q5FEL3_EHRRW	Q5fel3	ehrllichia r
712	80	5.7	1202	2	Q4WP24_ASPFU	Q4wp24	aspergillus	785	79.5	5.7	1591	2	Q5FFL1_EHRRG	Q5ffl1	ehrllichia r
713	80	5.7	1480	2	Q6CSL2_YARLI	Q6csl2	yarrowia li	786	79	5.7	154	2	Q42211_NECMA	Q42211	necturus ma
714	79.5	5.7	234	2	Q6JCS9_9HEMI	Q6jcs9	aleuropiatu	787	79	5.7	172	1	NU6M_PETWA	Q35544	petromyzo
715	79.5	5.7	235	2	Q5TRE9_SALCH	Q5tre9	salmonella	788	79	5.7	183	1	Y507_HAEIN	P44010	haemophilus
716	79.5	5.7	264	2	Q6ITH2_9TREM	Q6ith2	cercaria ba	789	79	5.7	183	2	Q4QN39_HAEI8	Q4qn39	haemophilus
717	79.5	5.7	264	2	Q6IT11_9TREM	Q6it11	cercaria ba	790	79	5.7	192	2	Q6CYK5_ERWCT	Q6cyk5	erwinia car
718	79.5	5.7	293	2	Q66D49_YERPS	Q66d49	yersinia ps	791	79	5.7	226	2	Q6HCD0_BACHK	Q6hcd0	bacillus th
719	79.5	5.7	296	2	Q91KCO_ERWCH	Q91kco	erwinia chr	792	79	5.7	229	2	Q8XIK9_CLOPE	Q8xik9	clostridium
720	79.5	5.7	296	2	Q6D4I7_ERWCT	Q6d4i7	erwinia car	793	79	5.7	248	2	Q50EH3_LACRE	Q50eh3	lactobacill
721	79.5	5.7	297	2	Q7U561_SYNFX	Q7u561	synecococc	794	79	5.7	278	2	Q5KL25_9ROSI	Q5kl25	populus tre
722	79.5	5.7	298	2	Q6CTH9_MOUSE	Q6cth9	kluyveromyc	795	79	5.7	282	2	Q4ULV8_RICFE	Q4ulv8	rickettsia
723	79.5	5.7	308	2	Q6CTH9_KLULA	Q6cth9	kluyveromyc	796	79	5.7	289	2	Q5U7L0_9PABA	Q5u7l0	glycyrrhiza
724	79.5	5.7	312	2	Q6ACY4_LEIXX	Q6acy4	leifsonia x	797	79	5.7	289	2	Q946J9_MCDTR	Q946j9	medicago tr
725	79.5	5.7	312	2	Q5AF82_CANAL	Q5af82	candida alb	798	79	5.7	293	1	Y543_CHLBN	Q9-809	chlamydia p
726	79.5	5.7	317	2	Q7UKZ3_RHOBA	Q7ukz3	rhodopirell	799	79	5.7	293	2	Q9KZD5_BACHD	Q9kdz5	bacillus ha
727	79.5	5.7	323	2	Q8DUD9_STRMU	Q8dud9	streptococc	800	79	5.7	300	2	Q6HM61_BACHK	Q6hm61	bacillus th
728	79.5	5.7	325	2	Q4NG89_9MICC	Q4ng89	arthroabacte	801	79	5.7	307	2	Q9JTQ9_NEIMA	Q9jtg9	neisseria m
729	79.5	5.7	329	2	Q4SJT4_TETNG	Q4sjt4	tetradodon n	802	79	5.7	310	2	Q8DAH5_VIBVU	Q8dah5	vibrio vuln
730	79.5	5.7	342	2	Q5KY68_GEOKA	Q5ky68	geobacillus	803	79	5.7	310	2	Q7MJN1_VIBVY	Q7mjn1	vibrio vuln
731	79.5	5.7	384	2	Q88ZD3_LACPL	Q88zd3	lactobacill	804	79	5.7	322	2	Q5P1V1_AZOSE	Q5p1v1	azocarcus sp
732	79.5	5.7	384	2	Q7NVC7_CHRVO	Q7nvc7	chromobacte	805	79	5.7	354	2	Q97C19_THEVO	Q97c19	thermoplas
733	79.5	5.7	405	2	Q77085_CABEL	Q77085	caenorhabdi	806	79	5.7	369	2	Q8PL40_XANAC	Q8pl40	xanthomonas
734	79.5	5.7	434	2	Q5E758_VIBF1	Q5e758	vibrio fisc	807	79	5.7	372	2	Q6GIA8_STAAR	Q6gia8	staphylococ
735	79.5	5.7	443	2	Q95AK6_9ASTR	Q95ak6	dialypetalu	808	79	5.7	373	2	Q8LBH3_ARATH	Q8lbh3	arabidopsis
736	79.5	5.7	445	2	Q55937_SYNY3	Q55937	synecocyst	809	79	5.7	377	2	Q9LXX8_ARATH	Q9lxx8	arabidopsis
737	79.5	5.7	445	2	Q6HKB2_BACHK	Q6hkb2	bacillus th	810	79	5.7	381	2	Q6FPD6_ACIAD	Q6fdd6	acinetobact
738	79.5	5.7	461	2	Q83RL6_SHIFL	Q83rl6	shigella fl	811	79	5.7	386	2	Q7NCK9_GLOVI	Q7nck9	gloeobacter
739	79.5	5.7	466	2	Q4WS19_ASPFU	Q4ws19	aspergillus	812	79	5.7	389	2	Q5L9Y3_BACFN	Q5l9y3	bacteroides
740	79.5	5.7	466	2	Q4KYL0_CAPBU	Q4kyl0	capsella bu	813	79	5.7	389	2	Q64Q89_BACFR	Q64q89	bacteroides
741	79.5	5.7	485	2	Q73Y55_MYCPA	Q73y55	mycobacteri	814	79	5.7	390	2	Q9X158_THEME	Q9x158	thermotoga
742	79.5	5.7	492	2	Q5H3W7_XANOR	Q5h3w7	xanthomonas	815	79	5.7	395	1	HNEB_ARCFU	Q29750	archaeoglob
743	79.5	5.7	499	2	Q9IYPI_PYPAB	Q9iyp1	pyrococcus	816	79	5.7	409	2	Q4IAN6_GIBZE	Q4ian6	gibberella
744	79.5	5.7	500	2	Q4NLS4_THEPA	Q4nls4	theileria p	817	79	5.7	409	2	Q6E830_9HEMI	Q6e830	potnia grad
745	79.5	5.7	505	2	Q93GK1_BACST	Q93gk1	bacillus st	818	79	5.7	410	1	Y588_BUCAI	P57648	buchnera ap
746	79.5	5.7	516	2	Q4NS64_9DELT	Q4ns64	anaeromyxob	819	79	5.7	414	2	Q66R30_YEAST	Q66r30	saccharomyc
747	79.5	5.7	517	2	Q6MY57_ASPFU	Q6my57	aspergillus	820	79	5.7	429	2	Q63YGB_BURPS	Q63ygb	burkholderi
748	79.5	5.7	531	2	Q51XQ2_MAGGR	Q51xq2	magnaporthe	821	79	5.7	438	2	Q7ACT1_ECO57	Q7act1	escherichia
749	79.5	5.7	535	2	Q4PKJ2_ORYSA	Q4pkj2	oryza sativ	822	79	5.7	439	2	Q8FGD5_ECOL6	Q8fgd5	escherichia
750	79.5	5.7	539	1	FIXN_AGR77	P98055	agrobacteri	823	79	5.7	439	2	Q4WKR6_ASPFU	Q4wkr6	aspergillus
751	79.5	5.7	542	2	Q577Q8_BRUAB	Q577q8	bruceella ab	824	79	5.7	442	2	Q4W667_VIBCH	Q4w667	vibrio chol
752	79.5	5.7	542	2	Q8FWF3_BRUSU	Q8fwf3	bruceella su	825	79	5.7	443	2	Q6LKM2_PROPR	Q6lkm2	photobacter
753	79.5	5.7	542	2	Q8YBWB_BRUME	Q8ybw8	bruceella me	826	79	5.7	444	2	Q7VT98_BORPE	Q7vt98	bordeatella
754	79.5	5.7	544	2	Q64940_9CORO	Q64940	avian infec	827	79	5.7	444	2	Q7W2C1_BORPA	Q7w2c1	bordeatella
755	79.5	5.7	559	2	Q51073_GEOKA	Q51073	geobacillus	828	79	5.7	444	2	Q7WR89_BORBR	Q7wr89	bordeatella
756	79.5	5.7	566	2	Q5SGW2_EMENI	Q5sgw2	aspergillus	829	79	5.7	444	2	Q8KKW1_VIBCH	Q8kkw1	vibrio chol
757	79.5	5.7	566	2	Q5SQN7_9HYME	Q5sqn7	perga conde	830	79	5.7	446	2	Q6L0U0_PICTO	Q6l0u0	picrophilus
758	79.5	5.7	570	2	Q8UF62_AGRIT5	Q8uf62	agrobacteri	831	79	5.7	447	2	Q6GER0_STAAR	Q6ger0	staphylococ
759	79.5	5.7	573	2	Q81V13_BACAN	Q81v13	bacillus an	832	79	5.7	453	2	Q8Y8B8_LISMO	Q8y8b8	listeria mo
760	79.5	5.7	573	2	Q63FV4_BACCCZ	Q63fv4	bacillus ce	833	79	5.7	456	2	Q9HID5_THEAC	Q9hid5	thermoplas
761	79.5	5.7	588	2	Q41543_GIBZE	Q41543	gibberella	834	79	5.7	456	2	Q7PB27_RICSI	Q7pb27	rickettsia

835	79	5.7	457	2	Q4NLS2_THEPA	Q4NLS2 theileria p	908	78.5	5.6	447	2	Q6CYW0_ERACT	Q6cyw0 erwinia car
836	79	5.7	464	2	Q8RC72_THETN	Q8rc72 thermoanaer	909	78.5	5.6	458	2	Q4HHT9_CAMCO	Q4hht9 campylobact
837	79	5.7	473	2	O16252_CABEL	O16252 caenorhabdi	910	78.5	5.6	464	2	Q979J8_THEVO	Q979j8 thermoplasm
838	79	5.7	479	2	O16926_CABEL	O16926 caenorhabdi	911	78.5	5.6	470	2	Q6C8J1_YARLI	Q6c8j1 yarrowia li
839	79	5.7	481	2	O629Y5_BURMA	O629y5 burkholderi	912	78.5	5.6	470	2	Q5N109_SYNP6	Q5n109 synechococc
840	79	5.7	489	2	Q97EE9_CLOAB	Q97ee9 clostridium	913	78.5	5.6	471	2	Q6AB86_PROAC	Q6ab86 propionibac
841	79	5.7	491	2	O4KH41_PSEF5	O4kh41 pseudomonas	914	78.5	5.6	474	2	Q4QK73_HAEI8	Q4qk73 haemophilus
842	79	5.7	492	2	Q5A405_CANAL	Q5a405 candida alb	915	78.5	5.6	478	2	Q5AY52_EMENI	Q5ay52 aspergillus
843	79	5.7	497	2	Q7TNN9_RAT	Q7tnn9 rattus norv	916	78.5	5.6	479	2	Q5GCA8_RHOGE	Q5gca8 rhodocyclus
844	79	5.7	498	2	Q4X148_ASPPU	Q4x148 aspergillus	917	78.5	5.6	482	2	Q83AAQ_COXBU	Q83aaq coxiellia bu
845	79	5.7	501	2	Q5TMB6_CHICK	Q5tmb6 gallus gall	918	78.5	5.6	483	2	Q85MF7_9NEOP	Q85mf7 cyreastis th
846	79	5.7	517	2	Q9XYS3_DICDI	Q9xys3 dictyosteli	919	78.5	5.6	493	2	Q9V0T0_PIRAB	Q9v0t0 pyrococcus
847	79	5.7	524	2	Q4W158_ASPPU	Q4w158 aspergillus	920	78.5	5.6	501	2	Q8FB10_ECOL6	Q8fb10 escherichia
848	79	5.7	526	2	Q4J830_SULAC	Q4j830 sulfolobus	921	78.5	5.6	510	2	Q9B8Y2_FASHE	Q9b8y2 fasciola he
849	79	5.7	534	2	Q88Z37_LACPL	Q88z37 lactobacill	922	78.5	5.6	512	2	Q6ZMD2_HUMAN	Q6zmd2 homo sapien
850	79	5.7	585	2	Q6OUU1_CAEBR	Q6ouu1 caenorhabdi	923	78.5	5.6	526	2	Q6MUB7_MYCMS	Q6mub7 mycoplasma
851	79	5.7	595	2	Q837Q4_ENTFA	Q837q4 enterococcu	924	78.5	5.6	559	2	Q6DCE3_XENLA	Q6dce3 xenopus lae
852	79	5.7	602	2	Q70X18_9META	Q70x18 rhyncholest	925	78.5	5.6	579	2	Q50465_MYCTU	Q50465 mycobacteri
853	79	5.7	658	2	Q6XJH8_9ERIC	Q6xjh8 sideroxylon	926	78.5	5.6	580	2	Q4MPJ8_BACCE	Q4mpj8 bacillus ce
854	79	5.7	658	2	Q6XJ12_9ERIC	Q6xj12 sideroxylon	927	78.5	5.6	583	2	Q950T2_HYACU	Q950t2 hyaloraphid
855	79	5.7	658	2	Q6XJL0_9ERIC	Q6xjl0 nesoluma po	928	78.5	5.6	591	2	Q88XJ9_DROPHI	Q88xj9 drosophila
856	79	5.7	669	1	NUSM_ARATH	P29188 arabidopsis	929	78.5	5.6	591	2	Q9V9U1_DROME	Q9v9u1 drosophila
857	79	5.7	682	2	Q6SU14_ORYSA	Q6su14 oryza sativ	930	78.5	5.6	622	1	COX1_BACSU	P24010 bacillus su
858	79	5.7	685	2	O19822_9LAMI	O19822 alseobla sp.	931	78.5	5.6	624	2	Q9LYR6_ARATH	Q9lyr6 arabidopsis
859	79	5.7	688	2	Q8MBX1_9ASTE	Q8mbx1 spheencoclea	932	78.5	5.6	641	2	Q5NM95_ZYMOO	Q5nm95 zymomonas m
860	79	5.7	692	2	Q9TIW2_9ASTE	Q9tiw2 phacelia ca	933	78.5	5.6	652	2	Q9TIX1_9ASTE	Q9tix1 codon schen
861	79	5.7	723	2	O35193_MOUSE	O35193 mus musculu	934	78.5	5.6	682	2	Q6USQ0_9DIPS	Q6uesq valeriana c
862	79	5.7	738	2	Q9TJS8_MORCI	Q9tjs8 morinda cit	935	78.5	5.6	691	2	Q93YK5_BRANA	Q93yk5 brassica na
863	79	5.7	746	2	Q9TLB7_DIGPU	Q9tlb7 digitalis p	936	78.5	5.6	732	2	Q98707_9GENT	Q98707 musaenda e
864	79	5.7	819	2	O31582_BACSU	O31582 bacillus su	937	78.5	5.6	732	2	Q9TJP6_9GENT	Q9tjp6 strumphia m
865	79	5.7	1501	2	O8CIQ9_MOUSE	O8ciq9 mus musculu	938	78.5	5.6	734	2	Q9TJQ0_9GENT	Q9tjq0 roglaria suf
866	79	5.7	1521	2	O8CGS3_MOUSE	O8cgs3 mus musculu	939	78.5	5.6	744	2	Q32645_MENTR	Q32645 menyanthes
867	79	5.7	1521	2	O8CIP6_MOUSE	O8cip6 mus musculu	940	78.5	5.6	779	2	Q6AGU5_PROAC	Q6aegu5 propionibac
868	79	5.7	1521	2	O8OZZ8_MOUSE	O8ozz8 mus musculu	941	78.5	5.6	798	2	O51M91_MAGGR	Q51m91 magnaporthe
869	79	5.7	1709	2	Q6LIW5_CAEBR	Q6liw5 caenorhabdi	942	78.5	5.6	825	2	Q6N215_RHOPE	Q6n215 rhodopeudo
870	79	5.7	1794	2	Q4QGV5_LEIMA	Q4qgv5 leishmania	943	78.5	5.6	863	2	Q92L62_RHIME	Q92l62 rhizobium m
871	79	5.7	2198	2	O18990_CABEL	O18990 caenorhabdi	944	78.5	5.6	864	2	Q4L5U5_STAHJ	Q4l5u5 staphylococ
872	78.5	5.6	169	2	Q7HSA7_HALSA	Q7hsa7 halobacteri	945	78.5	5.6	898	2	Q515C8_9TELE	Q515c8 cyprinid sp
873	78.5	5.6	241	1	MCBE_ECOLI	P05528 escherichia	946	78.5	5.6	1093	2	Q84W30_ARATH	Q84w30 arabidopsis
874	78.5	5.6	242	2	O6LPC6_PHOPR	O6lpc6 photobacter	947	78.5	5.6	1289	2	Q7RKA2_PLAYO	Q7rka2 plasmodium
875	78.5	5.6	254	2	Q4SVF4_TETNG	Q4svf4 tetraodon n	948	78.5	5.6	1325	2	O64533_ARATH	O64533 arabidopsis
876	78.5	5.6	264	2	O6ITH4_9TREM	O6ith4 cercaria ba	949	78.5	5.6	2556	2	Q9QH56_9ALPH	Q9qhn56 gallid herp
877	78.5	5.6	264	2	O6TIT2_9TREM	O6tit2 cercaria ba	950	78.5	5.6	3172	2	Q4QAV5_LEIMA	Q4qav5 leishmania
878	78.5	5.6	281	2	O5JU71_PYRKO	O5ju71 pyrococcus	951	78.5	5.6	4856	2	Q7PZB3_ANOGA	Q7pzb3 anopheles g
879	78.5	5.6	293	2	O4W8E1_9ACAR	O4w8e1 leptotrombi	952	78	5.6	158	2	Q9XW23_CABEL	Q9xw23 caenorhabdi
880	78.5	5.6	298	2	O65V25_MANSM	O65v25 manheimia	953	78	5.6	197	2	Q98CZ0_RHILO	Q98cz0 rhizobium l
881	78.5	5.6	298	2	Q73T54_MYCPA	Q73t54 mycobacteri	954	78	5.6	205	2	Q5VW88_HUMAN	Q5vw88 homo sapien
882	78.5	5.6	302	2	Q4L8C2_STAHL	Q4l8c2 staphylococ	955	78	5.6	209	2	Q4NBS5_DICDI	Q4nbs5 dictyosteli
883	78.5	5.6	314	2	Q970C7_SULTO	Q970c7 sulfolobus	956	78	5.6	227	2	Q8HMO0_9TELE	Q8hmj0 carapus bar
884	78.5	5.6	316	2	Q7EY23_ORYSA	Q7ey23 oryza sativ	957	78	5.6	231	2	Q5BL33_BRARE	Q5bl33 brachydanio
885	78.5	5.6	320	2	Q9BBU4_9MYRT	Q9bbu4 warneckea m	958	78	5.6	262	2	Q98A38_RHILO	Q98a38 rhizobium l
886	78.5	5.6	320	2	O7ZWS9_XENLA	Q7zws9 xenopus lae	959	78	5.6	268	2	O6LZ29_METMP	O6lzz9 methanococ
887	78.5	5.6	321	2	Q9BBV2_9MYRT	Q9bbv9 mouriri hel	960	78	5.6	295	2	Q6P8F8_XENTR	Q6pf8 xenopus tro
888	78.5	5.6	324	2	Q5F546_NEIG1	Q5f546 neisseria g	961	78	5.6	299	2	Q9QX34_MOUSE	Q9qx34 mus musculu
889	78.5	5.6	330	2	Q9MRZ1_9MYRT	Q9mrz1 heterocentr	962	78	5.6	307	2	Q9JYR8_NEIMB	Q9jyr8 neisseria m
890	78.5	5.6	335	2	Q9VU64_DROME	Q9vu64 drosophila	963	78	5.6	327	2	Q974Q0_SULTO	Q974q0 sulfolobus
891	78.5	5.6	340	2	O8G845_BIFLO	O8g845 bifidobacte	964	78	5.6	331	2	Q5JYA1_HUMAN	Q5jya1 homo sapien
892	78.5	5.6	356	2	O8DTT2_STEMU	O8dt2 streptococc	965	78	5.6	335	1	MRAY_CHLMU	Q9plg6 chlamydia m
893	78.5	5.6	366	1	Y1196_METUA	Q58596 methanococ	966	78	5.6	338	2	Q9KY69_STRCO	Q9ky69 streptomyce
894	78.5	5.6	389	2	Q93TD9_PSEYM	Q93td9 pseudomonas	967	78	5.6	340	2	Q7S3J4_NEUCR	Q7s3j4 neurospora
895	78.5	5.6	389	2	Q4ZWE3_PSESY	Q4zwe3 pseudomonas	968	78	5.6	353	2	Q8Q0J7_METNA	Q8q0j7 methanosarc
896	78.5	5.6	389	2	Q87WD8_PSESM	Q87wd8 pseudomonas	969	78	5.6	366	2	Q65F48_BACLD	Q65f48 bacillus li
897	78.5	5.6	393	2	Q639K7_BACCZ	Q639k7 bacillus ce	970	78	5.6	379	2	Q85L69_9TREM	Q85l69 chimaerohem
898	78.5	5.6	395	2	Q612Y3_CAEBR	Q612y3 caenorhabdi	971	78	5.6	382	2	Q92IS9_RICCN	Q92is9 rickettsia
899	78.5	5.6	397	2	Q8KW37_9RHOB	Q8kw37 ruegeria sp	972	78	5.6	388	2	Q5P1K0_AZOSE	Q5p1k0 azoarcus sp
900	78.5	5.6	397	2	Q5NHL1_FRATT	Q5nhl1 francisella	973	78	5.6	388	2	Q9RT25_DEIRA	Q9rt25 deinoxococcus
901	78.5	5.6	405	2	Q9U2M5_CABEL	Q9u2m5 caenorhabdi	974	78	5.6	392	2	Q9ESM5_RAT	Q9esm5 rattus norv
902	78.5	5.6	411	2	Q89ZC7_BACTN	Q89zc7 bacteroides	975	78	5.6	396	2	Q57MB7_SALCH	Q57mb7 salmoneella
903	78.5	5.6	412	2	Q7A856_STAAN	Q7a856 staphylococ	976	78	5.6	396	2	Q5PE30_SALPA	Q5pe30 salmoneella
904	78.5	5.6	412	2	Q9X884_STRAA	Q9x884 staphylococ	977	78	5.6	396	2	Q8Z581_SALTI	Q8z581 salmoneella
905	78.5	5.6	436	2	Q4K6F5_PSEF5	Q4kef5 pseudomonas	978	78	5.6	396	2	Q8ZSNJ7_SALTY	Q8zsnj7 salmoneella
906	78.5	5.6	443	2	Q57JMI_SALCH	Q57jmi salmoneella	979	78	5.6	408	2	Q81RH3_BACAN	Q81rh3 bacillus an
907	78.5	5.6	443	2	Q8Z1W4_SALTY	Q8z1w4 salmoneella	980	78	5.6	409	1	KCNK3_MOUSE	Q35111 mus musculu

981	78	5.6	409	2	Q6HZP9_BACAN	Q6h2p9 bacillus an	1054	77.5	5.6	335	2	Q9X0N3_THEME	Q9x0n3 thermotoga
982	78	5.6	409	2	Q6HJQ7_BACHK	Q6hj7 bacillus th	1055	77.5	5.6	347	2	Q7ORW1_9CETA	Q7orw1 berardius b
983	78	5.6	411	1	KCMK3_RAT	Q549i2 rattus norv	1056	77.5	5.6	359	2	Q6GDS8_STAAR	Q6gds8 staphylococ
984	78	5.6	414	1	YMB7_YEAST	Q04835 saccharomyc	1057	77.5	5.6	363	2	Q9YFU4_AERPE	Q9yfu4 aeropyrum p
985	78	5.6	416	2	Q5FLR6_LACAC	Q5flr6 lactobacilli	1058	77.5	5.6	367	2	Q67RR1_SYDTP	Q67rr1 symbiobacte
986	78	5.6	416	2	Q6VNS3_MOUSE	Q6vns3 mus musculu	1059	77.5	5.6	368	2	Q85GB7_CRYPTCHLAD	Q85gb7 cryptochlad
987	78	5.6	424	2	Q6SPZ8_9BACT	Q6sfz8 uncultured	1060	77.5	5.6	372	2	Q5AQX4_EMENI	Q5aqx4 aspergillus
988	78	5.6	428	2	Q6LS34_PHOPR	Q6ls34 photobacter	1061	77.5	5.6	386	2	Q4ZR77_PSEY	Q4zr77 pseudomonas
989	78	5.6	429	2	Q4LAB4_STAHJ	Q4lab4 staphylococ	1062	77.5	5.6	398	2	Q57PC1_SALCH	Q57pc1 salmonella
990	78	5.6	449	2	Q4HES6_CAMCO	Q4hes6 campylobact	1063	77.5	5.6	399	2	Q978I2_THERMOPLASM	Q978i2 thermoplasm
991	78	5.6	449	2	Q4HIV2_CAMLA	Q4hiv2 campylobact	1064	77.5	5.6	406	2	Q6DNG7_SOYBN	Q6dng7 glycine max
992	78	5.6	452	2	Q7VAQ3_PROMA	Q7vaq3 prochloroco	1065	77.5	5.6	406	2	Q4JZ96_STRPN	Q4jz96 streptococc
993	78	5.6	462	2	Q9Y8L1_PYRFU	Q9y8l1 pyrococcus	1066	77.5	5.6	436	2	Q8P6X7_BRARE	Q8p6x7 brachydanio
994	78	5.6	467	2	Q9SJD3_RABIT	Q9sjd3 oryctolagus	1067	77.5	5.6	443	2	Q8TRL4_METAC	Q8trl4 mechanosarc
995	78	5.6	474	2	Q8GKM7_STRAZ	Q8gkm7 streptomyc	1068	77.5	5.6	446	2	Q4NIG1_9MICC	Q4nig1 arthrobacte
996	78	5.6	486	2	Q8EGR6_SHEON	Q8egr6 shewanella	1069	77.5	5.6	448	2	Q9XMU9_TETRYMENA	Q9xmu9 tetrahymena
997	78	5.6	486	2	Q87F14_MOUSE	Q87f14 mus musculu	1070	77.5	5.6	458	2	Q6CZJ3_ERWCT	Q6czj3 erwinia car
998	78	5.6	490	2	Q8FP18_COREF	Q8fp18 corynebacte	1071	77.5	5.6	459	2	Q85UJ5_COTCH	Q85uj5 coturnix ch
999	78	5.6	495	2	Q6B9L4_MAIZE	Q6b9l4 zea mays (m	1072	77.5	5.6	460	2	Q7N370_PHOLL	Q7n370 photorhabdu
1000	78	5.6	498	2	Q8BVS0_MOUSE	Q8bvs0 mus musculu	1073	77.5	5.6	461	2	Q8X7F9_ECO57	Q8x7f9 escherichia
1001	78	5.6	517	2	Q98H22_RHILO	Q98h22 rhizobium l	1074	77.5	5.6	464	2	Q916G9_PSEAE	Q916g9 pseudomonas
1002	78	5.6	538	2	Q9JAE1_9PARA	Q9jae1 mumps virus	1075	77.5	5.6	477	2	Q87PF8_VIBPA	Q87pf8 vibrio para
1003	78	5.6	540	2	Q54IV7_DICDI	Q54iv7 dictyosteli	1076	77.5	5.6	477	2	Q8D9I1_VIBVU	Q8d9i1 vibrio vuln
1004	78	5.6	551	2	Q8BWG6_MOUSE	Q8bwg6 m mus muscu	1077	77.5	5.6	479	2	Q7MKV7_VIBVU	Q7mkv7 vibrio vuln
1005	78	5.6	553	2	Q6CQ66_KLULA	Q6cq66 klyveromyc	1078	77.5	5.6	479	2	Q7AEJ3_ECO57	Q7aej3 escherichia
1006	78	5.6	554	2	Q6NAP5_RHOPA	Q6nap5 rhodopseudo	1079	77.5	5.6	482	2	Q5KYK3_GSKOA	Q5kyk3 geobacillus
1007	78	5.6	565	2	Q9F3S8_RHOMR	Q9f3s8 rhodothermu	1080	77.5	5.6	492	2	Q7VFT5_HELHP	Q7vft5 helicobacte
1008	78	5.6	573	2	Q721X4_LEPIC	Q721x4 leptospira	1081	77.5	5.6	499	2	Q57JZ0_SALCH	Q57jz0 salmonella
1009	78	5.6	574	2	Q72T06_LEPIC	Q72t06 leptospira	1082	77.5	5.6	499	2	Q8Z3S3_SALTI	Q8z3s3 salmonella
1010	78	5.6	574	2	Q8F2F8_LEPIC	Q8f2f8 leptospira	1083	77.5	5.6	504	2	Q688L6_ORYSA	Q688l6 oryza sativ
1011	78	5.6	581	2	Q59TM8_CANAL	Q59tm8 candida alb	1084	77.5	5.6	507	2	Q7VSQ9_BORPE	Q7vsq9 bordetella
1012	78	5.6	581	2	Q59TR0_CANAL	Q59tr0 candida alb	1085	77.5	5.6	507	2	Q7WDH8_BORBR	Q7wdh8 bordetella
1013	78	5.6	585	2	Q59WN0_CANAL	Q59wn0 candida alb	1086	77.5	5.6	510	1	Y382_RICPR	Q9zde9 rickettsia
1014	78	5.6	587	2	Q4ZL77_PSESY	Q4zl77 pseudomonie	1087	77.5	5.6	510	2	Q9LE20_ARATH	Q9le20 arabidopsis
1015	78	5.6	658	2	Q6XJL1_9ERIC	Q6xjl1 neolemonie	1088	77.5	5.6	510	2	Q4MX86_BACCE	Q4mx86 bacillus ce
1016	78	5.6	659	2	Q5JB71_9ASPA	Q5jb71 babiana muc	1089	77.5	5.6	513	2	Q9KLS4_VIBCH	Q9kls4 vibrio chol
1017	78	5.6	662	2	Q4KTU5_PSEFF5	Q4ktu5 pseudomonas	1090	77.5	5.6	520	2	Q32477_JUSAM	Q32477 justicia am
1018	78	5.6	672	2	Q5JBAG_9ASPA	Q5jbag pscaudomys ci	1091	77.5	5.6	524	2	Q4LPV5_9BURK	Q4lpv5 burkholderi
1019	78	5.6	694	2	Q95677_SOLDU	Q95677 solanum dul	1092	77.5	5.6	526	2	Q55WR7_CRYNE	Q55wr7 cryptococcu
1020	78	5.6	701	2	O01843_CAEEL	O01843 caenorhabdi	1093	77.5	5.6	526	2	Q5KJ10_CRYNE	Q5kji0 cryptococcu
1021	78	5.6	806	2	Q4P678_USTMA	Q4p678 ustilago ma	1094	77.5	5.6	526	2	O81501_ARATH	O81501 arabidopsis
1022	78	5.6	808	2	Q5OV14_ENTHI	Q5ov14 entameoba h	1095	77.5	5.6	527	2	Q5ATG4_EMENI	Q5atg4 aspergillus
1023	78	5.6	830	2	O8PQAB_XANAC	O8pqab xanthomonas	1096	77.5	5.6	531	2	Q6YQU3_ONYPE	Q6yqu3 onion yello
1024	78	5.6	834	2	Q8E9A7_SHEON	Q8e9a7 shewanella	1097	77.5	5.6	532	1	COX1_RHOCA	Q98059 rhodobacter
1025	78	5.6	1333	2	Q4YU69_PLABE	Q4yu69 plasmodium	1098	77.5	5.6	535	2	Q55577_SYNY3	Q55577 synchocyst
1026	77.5	5.6	199	2	Q4QEX1_LEIMA	Q4qex1 leishmania	1099	77.5	5.6	612	2	Q76HH6_KATPE	Q76hh6 katsuwonus
1027	77.5	5.6	206	2	Q5KY19_GEOKA	Q5ky19 geobacillus	1100	77.5	5.6	612	2	Q85UE1_9SCOM	Q85ue1 eutymnus a
1028	77.5	5.6	212	2	O9KAJ4_BACHD	O9kaj4 bacillus ha	1101	77.5	5.6	617	2	Q7S080_NEUCR	Q7s080 neurospora
1029	77.5	5.6	229	2	O5UQ12_MIMIV	O5uq12 mimivirus.	1102	77.5	5.6	630	1	SC6A4_MACMU	Q9mx00 macaca mula
1030	77.5	5.6	243	2	Q93RC4_ECOLI	Q93rc4 escherichia	1103	77.5	5.6	635	2	Q9ASS7_ARATH	Q9ass7 arabidopsis
1031	77.5	5.6	260	2	Q7VV38_BORPE	Q7vv38 bordetella	1104	77.5	5.6	639	2	Q85L86_PISOC	Q85l86 pisaster oc
1032	77.5	5.6	260	2	Q7W0U7_BORPA	Q7w0u7 bordetella	1105	77.5	5.6	648	2	O8SLR2_COUGU	O8slr2 couroupita
1033	77.5	5.6	260	2	Q7WN67_BORBR	Q7wn67 bordetella	1106	77.5	5.6	649	2	O28449_ARCFU	O28449 archaeglob
1034	77.5	5.6	268	2	Q8U2B7_PYRFU	Q8u2b7 pyrococcus	1107	77.5	5.6	660	2	O6Y1T3_9LILI	O6y1t3 lachnanthes
1035	77.5	5.6	283	2	Q92WH1_RHIME	Q92wh1 rhizobium m	1108	77.5	5.6	665	2	Q9GGT9_9FOAL	Q9ggt9 dulichium a
1036	77.5	5.6	287	2	Q6KNJG_CORDI	Q6knjg corynebacte	1109	77.5	5.6	695	2	Q97A18_THEVO	Q97a18 thermoplasm
1037	77.5	5.6	288	2	Q9M4S9_ALLCE	Q9m4s9 allium cepa	1110	77.5	5.6	698	2	Q6BGZ2_DEBHA	Q6bgz2 debaryomyce
1038	77.5	5.6	288	2	Q9MF61_BETVU	Q9mf61 beta vulgar	1111	77.5	5.6	699	2	Q7YM04_9SOLA	Q7ym04 bdellovibri
1039	77.5	5.6	291	2	Q4HPK2_CAMUP	Q4hpk2 campylobact	1112	77.5	5.6	706	2	Q6MK05_DEBEA	Q6mk05 bdellovibri
1040	77.5	5.6	291	2	Q6ASD9_DESPS	Q6aad9 desulfotale	1113	77.5	5.6	717	1	PAL2_ARATH	P45724 arabidopsis
1041	77.5	5.6	292	2	Q721V7_LISMF	Q721v7 listeria mo	1114	77.5	5.6	717	2	Q8RWF4_ARATH	Q8rwp4 arabidopsis
1042	77.5	5.6	292	2	Q8Y8NC_LISMO	Q8y8nc listeria mo	1115	77.5	5.6	717	2	Q53ZM9_ARATH	Q53zm9 arabidopsis
1043	77.5	5.6	293	2	Q8BE98_PSEPK	Q8be98 pseudomonas	1116	77.5	5.6	750	2	Q93S90_XANCP	Q93s90 xanthomonas
1044	77.5	5.6	293	2	Q8ZGV5_YERPE	Q8zgv5 yersinia pe	1117	77.5	5.6	776	2	Q61N20_CAEER	Q61n20 caenorhabdi
1045	77.5	5.6	296	2	Q92ZHO_RHIME	Q92zho rhizobium m	1118	77.5	5.6	839	2	O8TQ74_METAC	O8tg74 methanosarc
1046	77.5	5.6	308	2	Q660J1_BORGA	Q660j1 borrelia ga	1119	77.5	5.6	855	2	O75AV9_ASHGO	O75av9 ashbya goss
1047	77.5	5.6	312	2	O7FR57_MOUSE	O7fr57 mus musculu	1120	77.5	5.6	861	2	Q89FW4_BRAJA	Q89fw4 bradyrhizob
1048	77.5	5.6	312	2	Q8VG20_MOUSE	Q8vg20 mus musculu	1121	77.5	5.6	870	1	GF155_HUMAN	Q7z3f1 homo sapien
1049	77.5	5.6	313	2	Q7E853_MOUSE	Q7e853 mus musculu	1122	77.5	5.6	870	2	Q4G0Y6_HUMAN	Q4g0y6 homo sapien
1050	77.5	5.6	317	2	Q8RFJ5_FUSNN	Q8rfj5 fusobacteri	1123	77.5	5.6	945	2	Q6FG02_ACTIAD	Q6fg02 acinetobact
1051	77.5	5.6	318	1	NULM_VARRU	Q94vc3 varanus rud	1124	77.5	5.6	953	1	CWH43_YEAST	P25618 saccharomyc
1052	77.5	5.6	321	2	Q94V12_VARGI	Q94v12 varanus gis	1125	77.5	5.6	1069	2	Q41VA6_AZOVI	Q41va6 azotobacter
1053	77.5	5.6	327	2	Q9MRZ6_9MYRT	Q9mrz6 comolia cor	1126	77.5	5.6	1118	2	Q9HUE7_PSEAE	Q9hue7 pseudomonas

1127	77.5	5-6	1402	1	Y02332_HUMAN	Q92628	homo sapien	1200	77	5-5	540	2	Q82SN0_NITEU	Q82sn0 nitrosomona
1128	77.5	5-6	1646	2	Q5B0U5_EMEIN	Q5b0u5 aspergillus	1201	77	5-5	551	1	FIXN_AZOCA	P98056 azorhizobii	
1129	77	5-5	181	2	Q82U94_PYRAE	Q8zu94 pyrobaculum	1202	77	5-5	551	2	Q73V35_MYCPA	Q73v35 mycobacteri	
1130	77	5-5	228	1	CRCB_METCA	Q606p3 methylococc	1203	77	5-5	552	2	Q81B60_BACCR	Q81b60 bacillus ce	
1131	77	5-5	262	2	Q8KJ17_RHILO	Q8kji17 rhizobium l	1204	77	5-5	579	2	Q8YSW1_ANASP	Q8ysw1 anabaena sp	
1132	77	5-5	269	2	Q73K03_TREDE	Q73k03 treponema d	1205	77	5-5	580	2	Q7PWG5_ANOGA	Q7pwg5 anopheles g	
1133	77	5-5	274	2	Q59KP1_CANAL	Q59kp1 candida alb	1206	77	5-5	581	2	Q5CXP4_CRYPV	Q5cxp4 cryptocspor	
1134	77	5-5	277	2	Q4MNV5_BACCE	Q4mnv5 bacillus ce	1207	77	5-5	586	2	Q5WYL4_LEGPL	Q5wyl4 legionella	
1135	77	5-5	282	2	Q73Q06_BACCL	Q73q06 bacillus ce	1208	77	5-5	588	2	Q6ALD0_DESPS	Q6ald0 desulfotale	
1136	77	5-5	282	2	Q720H2_LISMF	Q720h2 listeria mo	1209	77	5-5	597	2	Q6CLT4_KLULA	Q6clt4 kluyveromyc	
1137	77	5-5	282	2	Q8Y7M2_LISMO	Q8y7m2 listeria mo	1210	77	5-5	602	2	Q5QS04_POTTR	Q5qs04 potorous tr	
1138	77	5-5	284	2	Q21311_TETPY	Q21311 tetrahymena	1211	77	5-5	625	2	Q6SDA4_BACLD	Q6sda4 bacillus li	
1139	77	5-5	284	2	Q9T7M5_TETPY	Q9t7m5 tetrahymena	1212	77	5-5	639	2	Q4HBX7_9DEIO	Q4hbx7 deinoococcus	
1140	77	5-5	286	2	Q739X4_BACCL	Q739x4 bacillus ce	1213	77	5-5	662	1	CYOB_BUCAI	Q6g0v1 bartonella	
1141	77	5-5	293	2	Q82888_NITEU	Q82888 nitrosomona	1214	77	5-5	672	2	Q6G0V1_BARQU	Q6g0v1 lancea tibe	
1142	77	5-5	295	2	Q7YFS2_9HYME	Q7yfs2 neimaymex	1215	77	5-5	695	2	Q6H9F9_LANTI	Q6h9f9 vestia lyci	
1143	77	5-5	295	2	Q7YFS6_9HYME	Q7yfs6 nomaymex	1216	77	5-5	695	2	Q7YM01_9SOLA	Q7ym01 caenorhabdi	
1144	77	5-5	300	2	Q63EN6_BACCC	Q63en6 bacillus ce	1217	77	5-5	710	2	Q19239_CABEL	Q19239 caenorhabdi	
1145	77	5-5	302	2	Q81TX5_BACAN	Q81tx5 bacillus an	1218	77	5-5	716	2	Q8VXB0_ORYSA	Q8vxb0 oryza sativ	
1146	77	5-5	310	2	Q89YL4_BACTN	Q89yl4 bacteroides	1219	77	5-5	725	2	Q9TJP9_9GENT	Q9tjp9 spermacoce	
1147	77	5-5	314	2	Q7TRY1_MOUSE	Q7try1 mus musculu	1220	77	5-5	731	2	Q8MA29_9LAMI	Q8ma29 cyclocheilo	
1148	77	5-5	316	2	Q60UD5_CABBR	Q60ud5 caenorhabdi	1221	77	5-5	739	2	Q32109_9ASTR	Q32109 conyza sp.	
1149	77	5-5	318	2	Q5BU85_COLGU	Q5bu85 colobus gue	1222	77	5-5	749	2	Q83812_TREPA	Q83812 treponema p	
1150	77	5-5	318	2	Q5HLN5_STAEQ	Q5hln5 staphylococ	1223	77	5-5	778	2	Q6S2J4_ORYSA	Q6s2j4 oryza sativ	
1151	77	5-5	321	2	Q94VE3_VARME	Q94ve3 varanus mer	1224	77	5-5	785	1	POTS_ARATH	Q9m7k4 arabidopsis	
1152	77	5-5	332	2	Q92UP3_RHIME	Q92up3 rhizobium cl	1225	77	5-5	785	2	Q53X11_ARATH	Q53x11 arabidopsis	
1153	77	5-5	342	2	Q5WAH1_BACSK	Q5wah1 bacillus cl	1226	77	5-5	808	2	Q35190_MOUSE	Q35190 mus musculu	
1154	77	5-5	349	2	Q529R5_ORYSA	Q5z9r5 oryza sativ	1227	77	5-5	907	2	Q92P26_ARATH	Q92p26 arabidopsis	
1155	77	5-5	352	2	Q89SN1_BRAJA	Q89sn1 bradyrhizob	1228	77	5-5	915	2	Q9S7Y7_ARATH	Q9s7y7 arabidopsis	
1156	77	5-5	352	2	Q9W6K3_ANOCA	Q9w6k3 anolis caro	1229	77	5-5	922	2	Q5WNN4_CABBR	Q5wnn4 caenorhabdi	
1157	77	5-5	353	2	Q9TE65_9STRA	Q9t6e5 thalassione	1230	77	5-5	934	2	Q560L9_CRYNE	Q560l9 cryptococcu	
1158	77	5-5	354	2	Q6F2N6_ORYSA	Q6f2n6 oryza sativ	1231	77	5-5	934	2	Q5KPL5_CRYNE	Q5kpl5 cryptococcu	
1159	77	5-5	355	2	Q88DH5_PSEPK	Q88dh5 pseudomonas	1232	77	5-5	936	2	Q5DTE5_CABEL	Q5dte5 caenorhabdi	
1160	77	5-5	360	2	Q4SDK8_TETNG	Q4sdk8 tetraodon n	1233	77	5-5	978	2	Q5B7J1_EMENI	Q5b7j1 aspergillus	
1161	77	5-5	361	2	Q86JW2_DICDI	Q86jw2 dictyosteli	1234	77	5-5	1138	2	Q96VE8_SULTO	Q96ve8 sulfolobus	
1162	77	5-5	366	2	Q5LSX8_CHLAB	Q5lsx8 chlamydophi	1235	77	5-5	1176	2	Q6F749_ACIAD	Q6f749 acinetobact	
1163	77	5-5	369	2	Q556T9_DICDI	Q556t9 dictyosteli	1236	77	5-5	1240	2	Q8DKB8_SYNEL	Q8dkb8 synchococc	
1164	77	5-5	372	2	Q6DA40_ERWCT	Q6da40 erwinia car	1237	77	5-5	1556	2	Q4FYG2_LEIMA	Q4fyg2 leishmania	
1165	77	5-5	382	2	Q5E6G4_VIBF1	Q5e6g4 vibrio fisc	1238	77	5-5	1853	2	Q4W8R6_9COMO	Q4w8r6 gentian mos	
1166	77	5-5	386	2	Q4MX91_BACCE	Q4mx91 bacillus ce	1239	77	5-5	4706	2	Q9FN44_ARATH	Q9fn44 arabidopsis	
1167	77	5-5	387	2	Q891I6_BRAJA	Q89i16 bradyrhizob	1240	76.5	5-5	152	2	Q9YDP6_AERPE	Q9ydp6 aeropyrum p	
1168	77	5-5	390	2	Q4HML6_CAMLA	Q4hml6 campylobact	1241	76.5	5-5	175	2	Q81JTO_PLAF7	Q81jto plasmodium	
1169	77	5-5	390	2	Q7N821_PHOLL	Q7n821 photorhabdu	1242	76.5	5-5	243	2	Q8ZU92_PYRAE	Q8zu92 pyrobaculum	
1170	77	5-5	390	2	Q5WMD4_LEGPL	Q5wmd4 legionella	1243	76.5	5-5	259	2	Q90572_GINCI	Q90572 ginglymosto	
1171	77	5-5	390	2	Q5X556_LEGPA	Q5x556 legionella	1244	76.5	5-5	261	2	Q5E6M3_VIBF1	Q5e6m3 vibrio fisc	
1172	77	5-5	402	2	Q5Q036_ENTHI	Q5q036 entamoeba h	1245	76.5	5-5	262	1	CT142_HUMAN	Q8n6m3 homo sapien	
1173	77	5-5	403	2	Q9HJ33_THEAC	Q9hj33 thermoplasma	1246	76.5	5-5	263	2	Q5LYW5_STRT1	Q5lyw5 streptococc	
1174	77	5-5	416	2	Q5W5W1_9LACO	Q5w5w1 lactobacill	1247	76.5	5-5	263	2	Q5M3H8_STRT2	Q5m3h8 streptococc	
1175	77	5-5	417	2	Q97YX9_SULSO	Q97yx9 sulfolobus	1248	76.5	5-5	269	2	P96581_BACSU	P96581 bacillus su	
1176	77	5-5	438	1	SHIA_ECOLI	P76350 escherichia	1249	76.5	5-5	270	2	Q5WNP5_CABBR	Q5wnp5 caenorhabdi	
1177	77	5-6	438	2	Q34739_BACSU	Q34739 bacillus su	1250	76.5	5-5	272	2	Q5ETA2_9NEOP	Q5eta2 eueides tal	
1178	77	5-5	442	2	Q4ZUK0_PSEBSY	Q4zuko pseudomonas	1251	76.5	5-5	277	2	Q55T17_CRYNE	Q55t17 cryptococcu	
1179	77	5-5	451	2	Q73GR0_WOLPM	Q73gr0 wolbachia p	1252	76.5	5-5	284	1	FOCA_HAEIN	P43756 haemophilus	
1180	77	5-5	459	2	Q5Q831_MACLA	Q5q831 macroctis la	1253	76.5	5-5	284	2	Q4QP09_HAB18	Q4qp09 haemophilus	
1181	77	5-5	459	2	Q8SFC7_AREIN	Q8sfc7 arenaria in	1254	76.5	5-5	285	2	Q57PE2_SALCH	Q57pe2 salmonella	
1182	77	5-5	460	2	Q87GT8_VIBPA	Q87gt8 vibrio para	1255	76.5	5-5	285	2	Q4T685_TETNG	Q4t685 tetraodon n	
1183	77	5-5	461	2	Q73JZ7_TREDE	Q73jz7 treponema d	1256	76.5	5-5	289	2	Q22541_ORYSA	Q22541 oryza sativ	
1184	77	5-5	465	2	Q5JEY6_PYRKO	Q5jey6 pyrococcus	1257	76.5	5-5	292	2	Q61M86_CABBR	Q61m86 caenorhabdi	
1185	77	5-5	471	2	Q97U43_SULSO	Q97u43 sulfolobus	1258	76.5	5-5	300	1	F18F_ECO57	P69381 escherichia	
1186	77	5-5	475	2	Q5FSR4_GLUOX	Q5fsr4 gluconobact	1259	76.5	5-5	300	1	F1EF_ECOLI	P69380 escherichia	
1187	77	5-5	476	2	Q7T3R8_FUGRU	Q7t3r8 fugu rubrip	1260	76.5	5-5	301	2	Q23340_CABEL	Q23340 caenorhabdi	
1188	77	5-5	478	2	Q91WN3_MOUSE	Q91wn3 mus musculu	1261	76.5	5-5	301	2	Q4KSV5_VIBZE	Q4kvs5 vibrio chol	
1189	77	5-5	480	2	Q625W2_CABBR	Q625w2 caenorhabdi	1262	76.5	5-5	303	2	Q4IHF8_GIBZE	Q4ihf8 gibberella	
1190	77	5-5	485	2	Q87J14_VIBPA	Q87j14 vibrio para	1263	76.5	5-5	305	2	Q9KFT1_BACHD	Q9kft1 bacillus ha	
1191	77	5-5	486	2	Q6FLH2_CANGA	Q6flh2 candida gla	1264	76.5	5-5	307	2	Q4V9P1_BRARE	Q4v9p1 brachydanio	
1192	77	5-5	486	2	Q6GT48_BARHE	Q6gt48 bartonella	1265	76.5	5-5	308	2	Q4S377_TETNG	Q4s377 tetraodon n	
1193	77	5-5	496	2	Q4K039_STRPN	Q4k039 streptococc	1266	76.5	5-5	311	1	PAQR3_MOUSE	Q6tcg8 mus musculu	
1194	77	5-5	506	2	Q80XM3_MOUSE	Q80xm3 mus musculu	1267	76.5	5-5	311	2	Q6AXP7_RAT	Q6axp7 rattus norv	
1195	77	5-5	518	2	Q5UXT5_HALMA	Q5uxt5 haloarcula	1268	76.5	5-5	312	2	Q6PC57_BRARE	Q6pc57 brachydanio	
1196	77	5-5	519	1	SEC59_YEAST	P20048 saccharomyc	1269	76.5	5-5	319	2	Q6Q7V6_9MYRT	Q6q7v6 eriocnema f	
1197	77	5-5	527	2	Q6OPV5_CABBR	Q6opv5 caenorhabdi	1270	76.5	5-5	319	2	Q9YH55_CHICK	Q9yh55 gallus gall	
1198	77	5-5	532	2	Q8BCD0_PSEPK	Q8bcd0 pseudomonas	1271	76.5	5-5	321	2	Q9GEG8_9MYRT	Q9geg8 mouriri gui	
1199	77	5-5	536	2	Q8KJN9_RHILO	Q8kjin9 rhizobium l	1272	76.5	5-5	321	2	Q94VD1_9SAUR	Q94vd1 varanus pan	

1273	76.5	5.5	326	2	Q9GEH7_9MYRT	Q9geh7 heterocentr	1346	76.5	5.5	673	2	Q8HUT0_9ASPA	Q8huto dandya thad
1274	76.5	5.5	327	2	Q8DLE0_SYNEL	Q8dle0 synecococc	1347	76.5	5.5	675	2	Q8HUS1_9ASPA	Q8hus1 muilla clew
1275	76.5	5.5	332	2	Q4VAH2_MOUSE	Q4vah2 mus musculus	1348	76.5	5.5	677	2	Q6R3K6_ARATH	Q6r3k6 arabidopsia
1276	76.5	5.5	333	2	Q9MRX5_9MYRT	Q9mrx5 tibouchina	1349	76.5	5.5	681	2	Q51D78_ENTHI	Q51d78 entamoeba h
1277	76.5	5.5	334	2	Q9V056_PYRABX	Q9v056 pyrococcus	1350	76.5	5.5	681	2	Q5WLL8_BACSK	Q5wll8 bacillus cl
1278	76.5	5.5	339	2	Q7U0B3_SYNPX	Q7u0b3 synecoccc	1351	76.5	5.5	683	2	Q34302_RHET	Q34302 rhizobium e
1279	76.5	5.5	339	2	Q7VCR6_PROMA	Q7vcr6 prochloroco	1352	76.5	5.5	696	2	Q9TIV2_9ASTE	Q9tiv2 pholistoma
1280	76.5	5.5	344	1	TAR10_FAT	Q923y0 rattus norv	1353	76.5	5.5	705	2	Q9GHQ1_9ASTR	Q9ghq1 pseudonemac
1281	76.5	5.5	353	2	Q9TE67_9STRA	Q9te67 rhizosoleni	1354	76.5	5.5	716	2	Q6N428_RHOPA	Q6n428 rhodopseuo
1282	76.5	5.5	361	2	Q8AG37_CHICK	Q8ag37 gallus gall	1355	76.5	5.5	724	2	Q6FE05_ACIAD	Q6fe05 acinetobact
1283	76.5	5.5	369	2	Q8G6D1_BIFLO	Q8g6d1 bifidobacte	1356	76.5	5.5	725	1	YGL4_YEAST	P53134 saccharomyc
1284	76.5	5.5	370	2	Q8FZX1_BRUSU	Q8fzx1 brucella su	1357	76.5	5.5	727	2	Q8HTN8_9WAGN	Q8htn8 cocculus ca
1285	76.5	5.5	370	2	Q8YHY9_BRUME	Q8yhy9 brucella me	1358	76.5	5.5	729	2	Q96ND6_HUMAN	Q96nd6 homo sapien
1286	76.5	5.5	374	2	Q5TCF5_BRUAB	Q5tcf5 brucella ab	1359	76.5	5.5	734	2	Q9TJT3_9GENT	Q9tjt3 guettarda u
1287	76.5	5.5	382	2	Q85187_VIECH	Q85187 vibrio chol	1360	76.5	5.5	745	2	Q8WH81_9ASTE	Q8wh81 escallonia
1288	76.5	5.5	385	2	Q81Z31_HUMAN	Q81z31 homo sapien	1361	76.5	5.5	745	2	Q8WH88_9ASTE	Q8wh88 escallonia
1289	76.5	5.5	388	2	Q9N4S1_CABEL	Q9n4s1 caenorhabdi	1362	76.5	5.5	745	2	Q8WH91_9ASTE	Q8wh91 escallonia
1290	76.5	5.5	395	2	Q8Z700_SALTI	Q8z700 salmonella	1363	76.5	5.5	745	2	Q9MTH0_9ASTE	Q9mth0 escallonia
1291	76.5	5.5	395	2	Q8ZP15_SALTY	Q8zpi5 salmonella	1364	76.5	5.5	746	2	Q33117_9ASTR	Q33117 schlechtend
1292	76.5	5.5	396	2	Q9XDR1_ACTAC	Q9xdr1 actinobacil	1365	76.5	5.5	803	2	Q5C8V6_LEIMA	Q5c8v6 leishmania
1293	76.5	5.5	399	2	Q74HG7_LACJO	Q74hg7 lactobacill	1366	76.5	5.5	811	2	Q84MS3_ORISA	Q84ms3 oryza sativ
1294	76.5	5.5	404	2	Q81E11_BACCR	Q81e11 bacillus ce	1367	76.5	5.5	819	2	Q5SUS9_CRYNE	Q5sus9 cryptococcu
1295	76.5	5.5	419	2	Q638Y3_BACCC	Q638y3 bacillus ce	1368	76.5	5.5	819	2	Q5KHL0_CRYNE	Q5khl0 cryptococcu
1296	76.5	5.5	424	2	Q74M02_LACJO	Q74m02 lactobacil	1369	76.5	5.5	823	2	Q649F7_9ARCH	Q649f7 uncultured
1297	76.5	5.5	429	2	Q5WCR2_BACSK	Q5wcr2 bacillus cl	1370	76.5	5.5	834	2	Q4SPQ8_TETNG	Q4spq8 tetraodon n
1298	76.5	5.5	431	2	Q9K7K1_BACHD	Q9k7k1 bacillus ha	1371	76.5	5.5	855	2	Q9LZT7_ARATH	Q9lzt7 arabidopsis
1299	76.5	5.5	443	2	Q71XS7_LISMF	Q71xs7 listeria mo	1372	76.5	5.5	981	2	Q4ILH3_GIBZE	Q4ilh3 gibberella
1300	76.5	5.5	446	2	Q4U7F6_SULAC	Q4u7f6 sulfolobus	1373	76.5	5.5	1308	2	Q51W86_MAGGR	Q51w86 magnaporthe
1301	76.5	5.5	454	2	Q61JY2_CAEBR	Q61jy2 caenorhabdi	1374	76.5	5.5	1342	1	F7SK_ECO57	Q8x5h9 escherichia
1302	76.5	5.5	456	2	Q4W5B6_HUMAN	Q4w5b6 homo sapien	1375	76.5	5.5	2967	2	Q41892_9FLAV	Q41892 hepaticis g
1303	76.5	5.5	466	2	Q74HI0_LACJO	Q74hi0 lactobacil	1376	76.5	5.5	179	2	Q5IA42_AMEBC	Q5ia42 amborella t
1304	76.5	5.5	467	2	Q4HXS5_GIBZE	Q4hxs5 gibberella	1377	76	5.5	220	2	Q701X2_9CREN	Q701x2 uncultured
1305	76.5	5.5	474	1	PNTB_HAEIN	P43010 haemophilus	1378	76	5.5	216	2	Q632U0_BACCC	Q632u0 bacillus ce
1306	76.5	5.5	474	2	Q4U4B4_9GAMM	Q4u4b4 halomonas m	1379	76	5.5	256	2	Q4NFT8_9MICC	Q4nft8 arthrobacte
1307	76.5	5.5	475	1	HUTM_BACSU	P42087 bacillus su	1380	76	5.5	261	1	ZNUB_HAEIN	P44691 haemophilus
1308	76.5	5.5	476	2	Q57TP9_SALCH	Q57tp9 salmonella	1381	76	5.5	261	2	Q4QND6_HAEI8	Q4qnd6 haemophilus
1309	76.5	5.5	480	2	Q8ERF0_OCEIH	Q8erf0 oceanobacil	1382	76	5.5	275	2	Q97K81_CLOAB	Q97k81 clostridium
1310	76.5	5.5	480	2	Q5NHK8_FRATT	Q5nhk8 francisella	1383	76	5.5	275	2	Q891M8_CLOTE	Q891m8 clostridium
1311	76.5	5.5	486	2	Q8MPU6_CABEL	Q8mpu6 caenorhabdi	1384	76	5.5	277	2	Q634Q7_BACCC	Q634q7 bacillus ce
1312	76.5	5.5	495	2	Q8ZBT3_YERPE	Q8zbt3 yersinia pe	1385	76	5.5	277	2	Q64HDN7_BACHK	Q64hdn7 bacillus th
1313	76.5	5.5	495	2	Q66E75_YERPS	Q66e75 yersinia ps	1386	76	5.5	281	2	Q81LV5_BACAN	Q81lv5 bacillus an
1314	76.5	5.5	497	2	Q9HL81_THEAC	Q9hl81 thermoplas	1387	76	5.5	287	2	Q92CF3_LISIN	Q92cf3 listeria in
1315	76.5	5.5	498	2	Q5XCUB_STRP6	Q5xcub streptococc	1388	76	5.5	282	2	Q92180_RICCN	Q92i80 rickettsia
1316	76.5	5.5	498	2	Q9A0F5_STRP6	Q9a0f5 streptococc	1389	76	5.5	282	2	Q9CK77_PASMO	Q9ck77 pasteurella
1317	76.5	5.5	498	2	Q8P110_STRP8	Q8p110 streptococc	1390	76	5.5	286	2	Q81EN8_BACCR	Q81en8 bacillus ce
1318	76.5	5.5	498	2	Q8X803_STRP3	Q8x803 streptococc	1391	76	5.5	287	2	Q49874_LUPAL	Q49874 lupinus alb
1319	76.5	5.5	515	2	Q645E7_9SALA	Q645e7 oedipina po	1392	76	5.5	295	2	Q7YF89_9HYME	Q7yfe9 labidus coe
1320	76.5	5.5	518	2	Q6CLG6_KLULA	Q6clg6 kluyveromyc	1393	76	5.5	299	2	Q87JX9_VIBPA	Q87jx9 vibrio para
1321	76.5	5.5	538	2	Q5P8E9_AZOSE	Q5p8e9 azoarcus sp	1394	76	5.5	312	2	Q91ZC1_MOUSE	Q91zcl mus musculu
1322	76.5	5.5	541	1	AAP2_NEUCR	Q59942 neurospora	1395	76	5.5	316	2	Q8QRU3_9BETA	Q8qru3 pongine her
1323	76.5	5.5	546	2	Q4KIK2_PSEF5	Q4kik2 pseudomonas	1396	76	5.5	318	2	Q8CN93_STAEP	Q8cn93 staphylococ
1324	76.5	5.5	548	2	Q9YBH5_AERPE	Q9ybh5 aeropyrum p	1397	76	5.5	321	2	Q6SL25_9MAXI	Q6sl25 argulus ame
1325	76.5	5.5	560	2	Q5PIA5_AZOSE	Q5pia5 azoarcus sp	1398	76	5.5	325	2	Q8IQX1_DROME	Q8iqx1 drosophila
1326	76.5	5.5	568	2	Q6PML9_HUMAN	Q6pml9 homo sapien	1399	76	5.5	328	2	Q8GEH9_9MYRT	Q8geh9 dictaetanch
1327	76.5	5.5	568	2	Q9Y6R2_HUMAN	Q9y6r2 homo sapien	1400	76	5.5	336	2	Q21716_CABEL	Q21716 caenorhabdi
1328	76.5	5.5	568	2	Q8VTR9_ARATH	Q8vtr9 arabidopsis	1401	76	5.5	346	2	Q24MS8_DICDI	Q24ms8 dictyosteli
1329	76.5	5.5	569	2	Q5R4H0_PONPY	Q5r4h0 pongo pygma	1402	76	5.5	347	2	Q9VWK6_DROME	Q9vwk6 drosophila
1330	76.5	5.5	569	2	Q5RD54_PONPY	Q5rd54 pongo pygma	1403	76	5.5	353	2	Q8TE69_9STRA	Q8te69 fragilaria
1331	76.5	5.5	583	2	Q722T4_LISMF	Q722t4 listeria mo	1404	76	5.5	356	2	Q8D717_VIBVU	Q8d717 vibrio vuln
1332	76.5	5.5	596	2	Q5ZXP5_LEGPH	Q5zxp5 legionella	1405	76	5.5	361	1	MRAY_CHRVO	Q7np26 chromobacte
1333	76.5	5.5	602	2	Q5QS43_PSEPE	Q5qs43 pseudochair	1406	76	5.5	365	2	Q9KS99_VIBCH	Q9ks99 vibrio chol
1334	76.5	5.5	607	2	Q7LN57_ANDSE	Q7ln57 androsace s	1407	76	5.5	371	1	Y112B_HAEIN	Q86233 haemophilus
1335	76.5	5.5	626	2	Q94243_CABEL	Q94243 caenorhabdi	1408	76	5.5	373	2	Q6PDT2_ACIAD	Q6pdt2 acinetobact
1336	76.5	5.5	626	2	Q5HS19_STAEP	Q5hs19 staphylococ	1409	76	5.5	381	2	Q715Y5_BAITA	Q715y5 baionys tay
1337	76.5	5.5	626	2	Q8CWP0_STAEP	Q8cwp0 staphylococ	1410	76	5.5	384	2	Q6FS89_CANGA	Q6fse89 candida gla
1338	76.5	5.5	630	1	SC6A4_CAVPO	Q35899 cavia porce	1411	76	5.5	390	2	Q5ZVD3_LSGPH	Q5zvd3 legionella
1339	76.5	5.5	631	2	Q8HUU2_9ASPA	Q8huu2 bessera tui	1412	76	5.5	400	2	Q812J4_BACCR	Q812j4 bacillus ce
1340	76.5	5.5	640	2	Q9GEU2_9ERIC	Q9geu2 primula sik	1413	76	5.5	401	2	Q83NP3_TROW8	Q83np3 tropheryma
1341	76.5	5.5	656	2	Q5CTK4_CRYPV	Q5ctk4 cryptospori	1414	76	5.5	402	2	Q5R831_PONPY	Q5r831 pongo pygma
1342	76.5	5.5	661	2	Q9LBY2_SHEVI	Q9lby2 shewanella	1415	76	5.5	411	2	Q9XNZ5_9HYME	Q9xnz5 chelonus ep
1343	76.5	5.5	666	2	Q52732_RHET	Q52732 rhizobium e	1416	76	5.5	415	2	Q88A33_PSESM	Q88a33 pseudomonas
1344	76.5	5.5	669	2	Q8HUS3_9ASPA	Q8hus3 milla biflo	1417	76	5.5	415	2	Q915T3_PSEAE	Q915t3 pseudomonas
1345	76.5	5.5	672	2	Q8HUU3_9ASPA	Q8huu3 bessera ele	1418	76	5.5	418	2	Q6BYU7_DEBHA	Q6byu7 debaryomyce

1419	1	422	76	5.5	Q58916	methanococc
1420	2	424	76	5.5	Q81f43	bacillus ce
1421	2	429	76	5.5	Q6G1Z4	staphylococ
1422	2	430	76	5.5	Q6Y0P0	staphylococ
1423	2	430	76	5.5	Q6Y0P3	staphylococ
1424	2	430	76	5.5	Q63NH2	burkholderi
1425	2	430	76	5.5	Q62B98	burkholderi
1426	2	431	76	5.5	Q61W94	lactobacill
1427	2	432	76	5.5	Q61W93	eucalanus b
1428	2	433	76	5.5	Q92M74	rhizobium m
1429	2	433	76	5.5	Q4WQ21	aspergillus
1430	2	441	76	5.5	Q76M71	mus musculu
1431	1	444	76	5.5	Q42490	petromyzon
1432	2	447	76	5.5	Q9HPQ2	halobacteri
1433	2	452	76	5.5	P20049	saccharomyc
1434	2	452	76	5.5	Q6SFF4	unclutered
1435	2	453	76	5.5	Q721H6	lietaria mo
1436	2	457	76	5.5	Q7VUM3	bordetella
1437	2	457	76	5.5	Q7W1Z2	bordetella
1438	2	457	76	5.5	Q7WQX0	bordetella
1439	2	459	76	5.5	Q8W9B5	vombatus ur
1440	2	460	76	5.5	Q8HM18	caulophryne
1441	2	464	76	5.5	Q7QJ38	anopheles g
1442	2	465	76	5.5	Q51ZW8	magnaporthe
1443	2	467	76	5.5	Q6WRY0	xenopus tro
1444	2	470	76	5.5	Q8FAH1	escherichia
1445	2	472	76	5.5	Q5NVA3	pongo pygma
1446	2	473	76	5.5	Q4W9T9	aspergillus
1447	2	473	76	5.5	Q57HJ8	salmonella
1448	2	478	76	5.5	Q5KI12	geobacillus
1449	2	479	76	5.5	Q87134	vibrio chol
1450	2	480	76	5.5	Q912N9	pseudomonas
1451	2	492	76	5.5	Q6FEH2	acinetobact
1452	2	494	76	5.5	Q6FCO9	acinetobact
1453	2	495	76	5.5	Q8HCP7	oryza sativ
1454	2	495	76	5.5	Q6DB31	erwinia car
1455	2	497	76	5.5	Q7U380	bordetella
1456	2	499	76	5.5	Q5E8E8	vibrio fisc
1457	2	501	76	5.5	Q51Sx4	magnaporthe
1458	2	502	76	5.5	ACHA7	gallus gall
1459	2	502	76	5.5	NUZC	mesostigma
1460	2	509	76	5.5	Q643C9	streptomyce
1461	2	514	76	5.5	Q9CPB6	pasteurella
1462	2	518	76	5.5	Q6FLP3	candida gla
1463	2	520	76	5.5	Q82WY7	nitrosomona
1464	2	533	76	5.5	Q4OLG8	haemophilus
1465	2	536	76	5.5	Q98912	rhizobium l
1466	2	551	76	5.5	Q76M72	mus musculu
1467	2	554	76	5.5	Q89DA3	bradyrhizob
1468	2	558	76	5.5	P98002	paracoccuss
1469	2	570	76	5.5	Q9NS93	homo sapien
1470	2	572	76	5.5	Q4SD33	tetragon n
1471	2	573	76	5.5	Q6HNC4	bacillus th
1472	2	574	76	5.5	Q8DGC1	synecococc
1473	2	578	76	5.5	Q33024	ruellia gil
1474	2	580	76	5.5	Q85JB7	harporhytri
1475	2	585	76	5.5	Q5B1A2	aspergillus
1476	2	601	76	5.5	Q4WP94	aspergillus
1477	2	612	76	5.5	Q94T23	percopsis t
1478	2	617	76	5.5	Q45325	caenorhabdi
1479	2	622	76	5.5	Q9HEL3	neurospora
1480	2	635	76	5.5	Q51a83	silicibacte
1481	2	644	76	5.5	Q7S7W3	neurospora
1482	2	647	76	5.5	Q4T1V2	tetragon n
1483	2	648	76	5.5	Q9GEW8	manilkara z
1484	2	656	76	5.5	Q7Q103	anopheles g
1485	2	656	76	5.5	Q5NW11	azocarcus sp
1486	2	656	76	5.5	Q639D7	bacillus ce
1487	2	658	76	5.5	Q61E88	caenorhabdi
1488	2	658	76	5.5	Q4VVC5	vitellariop
1489	2	658	76	5.5	Q6XJM3	lecometodexa
1490	2	659	76	5.5	Q6CAT5	yarowia li
1491	2	659	76	5.5	Q8XBE6	escherichia

1492	76	5.5	663	2	Q6CW54	KLUJLA	Q6CW54	kluveromyc
1493	76	5.5	686	2	Q80WJ2	MOUSE	Q80WJ2	mus musculu
1494	76	5.5	695	2	Q32508	LYCCE	Q32508	lycium cest
1495	76	5.5	700	2	Q9SCG5	9ERIC	Q9SCG5	clavija int
1496	76	5.5	708	2	Q9THW7	9GENT	Q9THW7	mitrasacme
1497	76	5.5	719	2	Q6EMC0	LYCES	Q6EMC0	lycopersico
1498	76	5.5	724	2	Q7YX45	CABEL	Q7YX45	caenorhabdi
1499	76	5.5	738	2	Q8COP3	MOUSE	Q8COP3	mus musculu
1500	76	5.5	740	2	Q57RD3	SALCH	Q57RD3	salmonella

ALIGNMENTS

Q6UX65 HUMAN PRELIMINARY; PRT; 266 AA.

AC Q6UX65; Q86VD3;

DT 05-JUL-2004 (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)

DE WFO154 (Hypothetical protein MGS54289) (Novel protein).

GN Name=MGS54289; Synonyms=RP5-1180E21.1;

GN ORFNames=RP5-1180E21.1-001, UNQ154;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.B., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H., Yanaura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D., Wood W.I., Godowski P.J., Gray A.M.;

RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."

RL Genome Res. 13:2265-2270(2003).

RP [2]

RP NUCLEOTIDE SEQUENCE.

TX TISSUE=Brain, and Eye;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP [3]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Eye;

RG NIH MGC Project;


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RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Thomas D.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RL NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Director MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY358492; AAQ88856.1; -; mRNA.
DR EMBL; BC047025; AAH47025.3; -; mRNA.
DR EMBL; AL355816; CAI19366.1; -; Genomic_DNA.
DR EMBL; BC091509; AAH91509.1; -; mRNA.
DR Ensembl; ENSG00000156171; Homo sapiens.
KW Hypothetical prctein.
SQ SEQUENCE 266 AA; 29766 MW; 4F91D5C212D458E5 CRC64;

Query Match 100.0%; Score 1392; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 7.3e-108;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWFQOGLSFLPSALVIVTSAAFISYITAVTLHHIDPALPYISDTGTVAPKCLFGAML 60
DB 1 MWFQOGLSFLPSALVIVTSAAFISYITAVTLHHIDPALPYISDTGTVAPKCLFGAML 60

QY 61 NIAAVLCIATIIYRYKQVHALSPENVIKLNKAGLVILGILSCLGLSIVANFQKTTLPAA 120
DB 61 NIAAVLCIATIIYRYKQVHALSPENVIKLNKAGLVILGILSCLGLSIVANFQKTTLPAA 120

QY 121 HVSGAVLTFPGMSLYMFVQTILSYOMQPKIHGKQVFWIRLLLVICWGSALSMLTCSSVL 180
DB 121 HVSGAVLTFPGMSLYMFVQTILSYOMQPKIHGKQVFWIRLLLVICWGSALSMLTCSSVL 180

QY 181 HSGNFGTDLQKLNHPEDKGVLHMITTAAEWSMSFSFGFFFLTYIRDFQKISLRVEAN 240
DB 181 HSGNFGTDLQKLNHPEDKGVLHMITTAAEWSMSFSFGFFFLTYIRDFQKISLRVEAN 240

QY 241 LHGLTLYDTAPCPINNERTLLSRDI 266
DB 241 LHGLTLYDTAPCPINNERTLLSRDI 266

RESULT 3
QSCR48 MOUSE
ID Q9CR48 MOUSE PRELIMINARY; PRT; 267 AA.
AC Q9CR48;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610318G18 product:hypothetical protein, full
DE insert sequence (Mus musculus adult male tongue cDNA, RIKEN full-
DE length enriched library, clone:2310056E01 product:hypothetical
DE protein, full insert sequence) (Mus musculus 10 days lactation, adult
DE female mammary gland cDNA, RIKEN full-length enriched library,
DE clone:D730039103 product:hypothetical protein, full insert
DE sequence).
GN Name=2610318G18R1k;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaer P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;

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RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Glessi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kana A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zvolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RL [4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RL [5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sakai N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RL [6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Tongue, and Whole body;
RX Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Saeki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi P., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL [7]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi P., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyu T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK012044; BAB27990.1; -; mRNA.
DR EMBL; AK009940; BAB26598.1; -; mRNA.
DR EMBL; AK052824; BAC265162.1; -; mRNA.
DR Ensembl; ENSMUSG00000027900; Mus musculus.
DR MGI; MGI:1914421; 2610318G18Rik.
KW Hypothetical protein.
SQ SEQUENCE 267 AA; 30228 MW; 228214D5AFF36783 CRC64;
Query Match 89.4%; Score 1245; DB 2; Length 267;
Best Local Similarity 86.4%; Pred. No. 1.3e-95;
Matches 229; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
QY 1 MWMFOGSLFSLPSALVIMTSAFIPSYITAVTLHHIDPALPYISDTGTVAPEKCLPGML 60
DB 1 MWMFOGSLFSLPSALVIMTSAFIPSYITAVTLHHIDPALPYISDTGTTPPERCLFGVWL 60
QY 61 NIAAALCIATIIYVRYKQVHALSPENVIKLNKAGLVGLISCLGLSIVANFKTTLFAA 120
DB 61 NIAAALCIATIIYVRYKQVHALSPENVIKLNKAGLVGLISCLGLSIVANFKTTLFIV 120
QY 121 HVSGAVLTFMGSLYMFVQTILSYQMPKIHKQVFWIRLLLVWCGVSALSMLTSSVL 180
DB 121 HVCGAVLAFSMGSLYMFVQTILSYQMPKIHKQVFWIRLLLVWCGVSALSMLTSSVL 180
QY 181 HSGNFGTDLCKLHNPDKGVLHMTTAAEWSMSPFPGFGLTYIRDFOKISLREAN 240
DB 181 YSSDFGPDVQKLLHNPDKGVLHMTTAAEWSMSPFPGFGLTYIRDFOKITURVEAN 240
QY 241 LHGLTYLDTAPCPINNERTLLSRD 265
DB 241 LHGLTYLDTAPCPINNERTLLSRD 265
RESULT 4
Q5BK09_RAT PRELIMINARY; PRT; 267 AA.
AC Q5BK09;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein LOC362011.
GN Name=LOC362011;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
TX TISSUE=Liver;
RX MEDLINE=23888257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091251; AAH91251.1; -; mRNA.
RW Hypothetical protein.
SQ SEQUENCE 267 AA; 30173 MW; 5B8D99C7A8B018E1 CRC64;

Query Match 88.8%; Score 1236; DB 2; Length 267;
Best Local Similarity 86.0%; Pred. No. 7.4e-95;
Matches 228; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWFQOGLSFLPSALVIWTSAAPIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MWFQOGLSFLPSALVIWTFATFISYITAITLHVDPALPYISDTGTPPSPCLFGVNL 60

QY 61 NTAANLCIATIIYVRVQVHALSPENVIILKNKAGVLGLSCLGISIVANFQKTLFPA 120
DB 61 NTAANVLGIATIIYVRVQVHALPENLIIILKNKAGLVGLSCLGLSLVNFQKSLFTV 120

QY 121 HVSGAVLTFMGSLYFVQTILSYQWPKIHQKQVFWIRLLLVIVCGVSALSMVLCSSVL 180
DB 121 HVCQAVLAFSMGSLYFVQTILSYQWPKIHQKQVFWIRLLLVIVCGVSALSMVLCSSVL 180

QY 181 HSGNFGTDLQKLNHPDKGVLLHMTTAAWSMSFSPFGFLYIRDPFKISIRVRAN 240
DB 181 YSSDFGADIVQKLNHPDKGVLLHMTTAAWSMSFSPFGFLYIRDPFKISIRVRAN 240

QY 241 LHGLTLTYDPAFCPINNRPRLLSRD 265
DB 241 LHGLTLTYDPAFCPVNTPPLLSRD 265

RESULT 5
QD520_MOUSE PRELIMINARY; PRT; 267 AA.
AC QD520;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4930524M19 product:hypothetical protein, full insert
DE sequence.
GN Name=2610318G18R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=103496316; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085860; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino H., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu F., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The PANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=204959374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK015888; BAB30020.1; -; mRNA.
DR Ensembl; ENSMUSG00000027900; Mus musculus.
RW MGI; MGI:1914421; 2610318G18R1k.
KW Hypothetical protein.
SQ SEQUENCE 267 AA; 30244 MW; 228214D5AFF37CEF CRC64;

Query Match 88.7%; Score 1235; DB 2; Length 267;
Best Local Similarity 86.0%; Pred. No. 8.9e-95;
Matches 228; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 MWFQOGLSFLPSALVIWTSAAPIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

QY

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Db      1  MMWFOOGLSFLPALVIWTFATIFSYITAITLHVDPALPYISDGTTPPERCLFGVML 60
QY      61  NIAAVLCIATVYRYKQVHALSPEENVIIKLNKAGLVGLTSLCGLSIVANFOKTLFAA 120
Db      61  NIAAVLGATWYRYKQVHALSPEENVIIKLNKAGLVGLTSLCGLSIVANFOKTLFIV 120
QY      121  HVSGAVLTGMSGLYNFVOTILSYQYQPKIHGQVFWIRLLLVWCVGSALSMLTCSYVL 180
Db      121  HVCGAVLAFSMGSGFYMFVOTILSYQYQPKIHGQVFWIRLLLVWCVGSALSMTCSIL 180
QY      181  HSGNFTGLEOKLHNPBKGVLHMTTAAEWSMSFSFGPGLTIVIRFQKISLRYEAN 240
Db      181  YSDFGPDVQVQLHWPBKGVLHMTTAAEWSMSFSFGPGLTIVIRFQKISLRYEAN 240
QY      241  LHGLTLYDTAPCPINNERTLLSRD 265
Db      241  LHGLTLYDTVPCLVNNERTPLSRD 265

RESULT 6
Q9D835_MOUSE PRELIMINARY; PRT; 180 AA.
ID Q9D835;
AC Q9D835;
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Mus musculus adult male small intestine cDNA, RIKEN full-length
DE enriched library, clone:2010305N14 product:hypothetical protein, full
DE insert sequence (2610318G18Rik protein).
GN Name:2610318G18Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuura H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo S., Nishida K., Nomura K., Numazaki R., Ohno M.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kameya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=22354689; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

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RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brucic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shinada M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watehiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed capillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori P.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

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RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,						
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,						
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,						
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,						
RA	Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,						
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,						
RA	Villaola D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,						
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,						
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,						
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,						
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,						
RA	Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalus D.B.,						
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;						
RT	"Generation and initial analysis of more than 15,000 full-length human						
RT	cDNA sequences.";						
RP	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).						
RN	[8]						
RP	NUCLEOTIDE SEQUENCE.						
RC	STRAIN=FVB/N; TISSUE=Kidney;						
RA	Straubberg R.;						
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; AK008532; BAB25725.1; -; mRNA.						
DR	EMBL; BC024458; AAH24458.1; -; mRNA.						
DR	Ensembl; ENSMUSG00000027900; Mus musculus.						
DR	MGI; MGI:1914421; 2610318I8Rik.						
KW	Hypothetical protein.						
SQ	SEQUENCE 180 AA; 20324 MW; 7952C2302D9235DF CRC64;						
Query Match	57.9%; Score 805.5; DB 2; Length 180;						
Best Local Similarity	60.0%; Pred. No. 3.7e-59;						
Matches 159; Conservative	12; Mismatches 7; Indels 87; Gaps 1;						
QY	1 MWVFQQGLSFLPSALVITWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFCAML	60					
Db	1 MWVFQQGLSFLPSALVITWTATFIFSYITAITLHVDPALPYISDTGTIIIPERCLFGVML	60					
QY	61 NIAAVLCIATIYRYKVQKHVALSPENVIIKLNKAGLVGLSCIGLSIVANFOKTTLFAA	120					
Db	61 NIAAVLGIAITMYRYKVQKHVALNPENLIILKNKAGLVGLSCIGLSLVANFO	113					
QY	121 HVSGAVLTFGNGSLYMFQTILSYQMOPKTHGKOVFIIRLLLVTCWGVSALSMLTCSVL	180					
Db	114 -----GVVHLVHTVTAAWSMSFFGFITYIRDFOKISRVEAN	113					
QY	181 HSGNFGTDLEQKLNHPEDKYVLHMITTAAWSMSFFGFITYIRDFOKISRVEAN	240					
Db	114 -----GYVHLVHTVTAAWSMSFFGFITYIRDFOKITLRVEAN	153					
QY	241 LHGLTYDTAPCPINNERTLLSRD	265					
Db	154 LHGLTYDTVPCCVNNERTPLLRSD	178					

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RESULT 7
Q6IQIO BRARE
ID Q6IQIO BRARE PRELIMINARY; PRT; 272 AA.
AC Q6IQIO;
DT 05-JUN-2004 (TREMBlrel. 27, Created)
DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)
ZGC:86754.
ORFNames=zgc:86754;
GN Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
{1}
RN
RP NUCLEOTIDE SEQUENCE..
RC
RC TISSUE=Embryo;
RX MDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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[illegible]

RT Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-
 RT Capped cDNA Libraries."
 RL DNA Res. 12:117-126(2005).
 DR EMBL; AK075350; BAC11562.1; -; mRNA.
 SQ SEQUENCE 136 AA; 15728 MW; 984FEDC29636AC0C CRC64;

Query Match 52.1%; Score 725; DB 2; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.4e-52;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 MGSLYNFVOTILSYOMQPKIHGKQVFWIRLLVIMCGVSALSMLTSCSSVLHSGNFGTDLE 190
 DB 1 MGSLYNFVOTILSYOMQPKIHGKQVFWIRLLVIMCGVSALSMLTSCSSVLHSGNFGTDLE 60

QY 191 OKLHWNPEDKGYLVHMITTAAEWSMSFSFGFPLTYIRDFQKISLRVEANLHGLTIYDTA 250
 DB 61 OKLHWNPEDKGYLVHMITTAAEWSMSFSFGFPLTYIRDFQKISLRVEANLHGLTIYDTA 120

QY 251 PCPINNERTLLSRDI 266
 DB 121 PCPINNERTLLSRDI 136

RESULT 9
 Q8N682 HUMAN
 ID Q8N682 HUMAN PRELIMINARY; PRT; 238 AA.
 AC Q8N682;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE FLJ11259 protein.
 GN Name=FLJ11259;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toshnyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RL Director MGC Project;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018435; AAH18435.1; -; mRNA.
 DR Ensembl; ENSG00000136048; Homo sapiens.
 SQ SEQUENCE 238 AA; 26253 MW; 51107567737F6C0 CRC64;

Query Match 35.4%; Score 492.5; DB 2; Length 238;
 Best Local Similarity 38.8%; Pred. No. 6.2e-33;
 Matches 97; Conservative 53; Mismatches 79; Indels 21; Gaps 3;

QY 1 MWWFOGLSFLPSALVIMTSAAFIFSITPAVTLHHIDPALPYISDTGTVPAPKCLFGAML 60
 DB 1 MLCFLRGMAFVFLVLTWSSAAFIISYVAVLSGHVNPFLPYISDTGTPPESGIFGMI 60

QY 61 NTAAVLCIATIVRYKQV-----HALSPENVIKLNKAGLVGLISCLGLSIVANFQ 113
 DB 61 NFSALGATMYTRYKIVOKQNTCTYFSTPVENLV-----SLVLGLVCGFGMIVANFQ 114

QY 114 KTTLLFAAHVSGAVLFGMGLYMFQVTLISYOMQPKIHGKQVFWIRLLVIMCGVSALS 173
 DB 115 ELAVPVHDDGALLAFVCGVYVTLTQSIISYKSCQWNSLSTCHIRMWISAVSCAIVPM 174

QY 174 LTCSSVLHSGNFGTDLEOKLHWNPEDKGYLVHMITTAAEWSMSFSFGFPLTYIRDFQKI 233
 DB 175 IVCASLISI-----TKLEWNPREDVYVHVWSAICWTVAFGFIFFLTFIQDFQSV 226

QY 234 SLRVEANLHG 243
 DB 227 TLRISTEING 236

RESULT 10
 Q9DC58 MOUSE
 ID Q9DC58 MOUSE PRELIMINARY; PRT; 238 AA.
 AC Q9DC58;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
 DE clone:120002N14 product:hypothetical RNA-binding region RNP-1 (RNA
 DE recognition motif) containing protein, full insert sequence.
 GN Name=120002N14RIK;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RA The FANTOM Consortium,


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RESULT 12
QSRGJ7 BRARE PRELIMINARY; PRT; 240 AA.
ID QSRGJ7 BRARE PRELIMINARY; PRT; 240 AA.
AC QSRGJ7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein.
GN Names=OTTDP00000008145; ORFNames=CH211-234F20.4-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Clark S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX890572; CA11845.1; -; Genomic DNA.
SQ SEQUENCE 240 AA; 27111 MW; 4A50CE578A2F24D7 CRC64;

Query Match 34.2%; Score 476.5; DB 2; Length 240;
Best Local Similarity 39.7%; Pred. No. 1.3e-31;
Matches 96; Conservative 43; Mismatches 94; Indels 9; Gaps 3;

QY 1 MWFQOGLSLPSALVITWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MWFMEGMCLPPTFLVWSSSTFIISYIALYRQDVVDVLPYISDTGATPPESCIVFGFMS 60
QY 61 NIAVLCIATIVYRYQVHALSPENVI-IKLNKAGLVIGILSCGLSIVANFQKTLTFLA 119
DB 61 TITAFAPAFATYAEYKFERVHERTGAVPTLNKVSFGFICIGICLVATVQETTVME 120
QY 120 AHVSGAVLTFMGSLYMFVQITLSYQMPKIHGQVFWIRLLVIVCGVSALSMLTCSVV 179
DB 121 VHDIGALLFPICGVYAVIQSVIGYAFYVGGSKFMCHLRTFFSTVAIIAAPIACGFL 180
QY 180 LHSNGFCTDLEQKLHNPEDKGYVLHMITTAAEWSMSFSGFGLTYIRDFQKISLRVEA 239
DB 181 V-----GT---SKLWDSNDKDYTRIHSVACIEWITTFSFVFLFYIQEFQOFTLKLTIV 232
QY 240 NL 241
DB 233 NL 234)
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RESULT 13
QSEAK8 XENTR PRELIMINARY; PRT; 239 AA.
ID QSEAK8 XENTR PRELIMINARY; PRT; 239 AA.
AC QSEAK8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE MGC108229 protein.
GN Names=MGC108229;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tissue=Whole body;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany P.H.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Klein S., Gerhard D.S.;
RC Tissue=Whole body;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC090386; AAH90386.1; -; mRNA.
SQ SEQUENCE 239 AA; 26578 MW; 2504EC8C84A34DA8 CRC64;

Query Match 34.0%; Score 473.5; DB 2; Length 239;
Best Local Similarity 39.4%; Pred. No. 2.4e-31;
Matches 95; Conservative 55; Mismatches 82; Indels 9; Gaps 4;

QY 3 WFOQGLSLPSALVITWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI 62
DB 4 WCLHGAAPLPSILVWSSAGFLFSYIISVLIGHVPPFPYISDTGTSPESGVFGPMISL 63
QY 63 AAVLCIATIVYRYQVHALSPENVI-IKLNKAGLVIGILSCGLSIVANFQKTLTFLA 121
DB 64 SAMLGAATMYTRYKILEKQNHSTDFLPYFYVTSLSAIGLIGCMGIVATFOEMAYPAVH 123
QY 122 VSGAVLTFMGSLYMFVQITLSYQMPKIHGQVFWIRLLVIVCGVSALSMLTCSVLH 181
DB 124 DAGALITFCGVLYILLQSYISYKSCPANTRVTCIRMAISVIAFIVPM-SVFSVL- 181
QY 182 SGNFGCTDLEQKLHNPEDKGYVLHMITTAAEWSMSFSGFGLTYIRDFQKISLRVEANL 241
DB 182 SG-----RKRLDWKPSDEGYHVLTSALCEIVAFGFMNYFLTFTRDQGVSIQISTEI 235
QY 242 H 242
DB 236 H 236

RESULT 14
QENRS6 XENLA PRELIMINARY; PRT; 287 AA.
ID QENRS6 XENLA PRELIMINARY; PRT; 287 AA.
AC QENRS6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC431986 protein (Fragment).
GN Name=LOC431986;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tissue=Liver;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany P.H.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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